

GenCore version 5.1.4_p5_4578
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OM protein - protein search, using sw model

Run on: May 6, 2003, 10:17:10 ; Search time 35 Seconds
(without alignments)
22.843 Million cell updates/sec

Title: US-09-555-115a-66

Perfect score: 43

Sequence: 1 CCGKTC 6

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: /SID52/gcgdata/geneseq/emb1/AA1980.DAT:*
2: /SID52/gcgdata/geneseq/emb1/AA1981.DAT:*
3: /SID52/gcgdata/geneseq/emb1/AA1982.DAT:*
4: /SID52/gcgdata/geneseq/emb1/AA1983.DAT:*
5: /SID52/gcgdata/geneseq/emb1/AA1984.DAT:*
6: /SID52/gcgdata/geneseq/emb1/AA1985.DAT:*
7: /SID52/gcgdata/geneseq/emb1/AA1986.DAT:*
8: /SID52/gcgdata/geneseq/emb1/AA1987.DAT:*
9: /SID52/gcgdata/geneseq/emb1/AA1988.DAT:*
10: /SID52/gcgdata/geneseq/emb1/AA1989.DAT:*
11: /SID52/gcgdata/geneseq/emb1/AA1990.DAT:*
12: /SID52/gcgdata/geneseq/emb1/AA1991.DAT:*
13: /SID52/gcgdata/geneseq/emb1/AA1992.DAT:*
14: /SID52/gcgdata/geneseq/emb1/AA1993.DAT:*
15: /SID52/gcgdata/geneseq/emb1/AA1994.DAT:*
16: /SID52/gcgdata/geneseq/emb1/AA1995.DAT:*
17: /SID52/gcgdata/geneseq/emb1/AA1996.DAT:*
18: /SID52/gcgdata/geneseq/emb1/AA1997.DAT:*
19: /SID52/gcgdata/geneseq/emb1/AA1998.DAT:*
20: /SID52/gcgdata/geneseq/emb1/AA1999.DAT:*
21: /SID52/gcgdata/geneseq/emb1/AA2000.DAT:*
22: /SID52/gcgdata/geneseq/emb1/AA2001.DAT:*
23: /SID52/gcgdata/geneseq/emb1/AA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	43	100.0	6	20	AAV06261
2	39	90.7	779	22	ABR66318
3	38	88.4	33	21	ABR09028
4	38	88.4	232	21	AAV0923
5	37	86.0	27	23	ABR6741
6	37	86.0	27	23	ABR6846
7	37	86.0	33	23	ABR09013
8	37	86.0	33	23	ABR09014
9	37	86.0	33	23	ABR09015
10	37	86.0	33	23	ABR09016

11	37	86.0	33	23	ABR09017	Imperatoxin linear
12	37	86.0	33	23	ABR09018	Imperatoxin linear
13	37	86.0	33	23	ABR09019	Imperatoxin linear
14	37	86.0	33	23	ABR09020	Imperatoxin linear
15	37	86.0	33	23	ABR09021	Imperatoxin linear
16	37	86.0	33	23	ABR09022	Imperatoxin linear
17	37	86.0	33	23	ABR09023	Imperatoxin linear
18	37	86.0	33	23	ABR09024	Imperatoxin linear
19	37	86.0	33	23	ABR09025	Imperatoxin linear
20	37	86.0	33	23	ABR09026	Imperatoxin linear
21	37	86.0	33	23	ABR09027	Imperatoxin linear
22	37	86.0	33	23	ABR09028	Imperatoxin linear
23	37	86.0	33	23	ABR09029	Imperatoxin linear
24	37	86.0	33	23	ABR09030	Imperatoxin linear
25	37	86.0	33	23	ABR09031	Imperatoxin linear
26	37	86.0	33	23	ABR09032	Imperatoxin linear
27	37	86.0	33	23	ABR09033	Imperatoxin linear
28	37	86.0	33	23	ABR09034	Imperatoxin linear
29	37	86.0	33	23	ABR09035	Imperatoxin linear
30	37	86.0	33	23	ABR09036	Imperatoxin linear
31	37	86.0	33	23	ABR09037	Imperatoxin linear
32	37	86.0	33	23	ABR09038	Imperatoxin linear
33	37	86.0	33	23	ABR09039	Imperatoxin linear
34	37	86.0	33	23	ABR09040	Imperatoxin linear
35	37	86.0	33	23	ABR09041	Imperatoxin linear
36	37	86.0	33	23	ABR09042	Imperatoxin linear
37	37	86.0	33	23	ABR09043	Imperatoxin linear
38	37	86.0	33	23	ABR09044	Imperatoxin linear
39	37	86.0	33	23	ABR09045	Imperatoxin linear
40	37	86.0	33	23	ABR09046	Imperatoxin linear
41	37	86.0	33	23	ABR09047	Imperatoxin linear
42	37	86.0	33	23	ABR09048	Imperatoxin linear
43	37	86.0	33	23	ABR09049	Imperatoxin linear
44	37	86.0	33	23	ABR09050	Imperatoxin linear
45	37	86.0	33	23	ABR09051	Imperatoxin linear

ALIGNMENTS

XX	RESULT 1
XX	AAV06261
ID	AAV06261 standard; Peptide; 6 AA.
XX	
AC	AAV06261;
XX	
DT	23-AUG-1999 (first entry)
XX	
DE	Staphylococcal enterotoxin mutant SEC1-12 loop deletion region
XX	
KW	Enterotoxin; SEC1; toxin; disulfide loop; protein engineering;
KM	mutant.
XX	
OS	Staphylococcus aureus.
OS	Synthetic.
XX	
PN	WO927889-A2.
XX	
PD	10-JUN-1999.
XX	
PF	01-DEC-1998; 98WO-US25107.
XX	
PR	02-DEC-1997; 97US-0067357.
XX	
PA	(IDAH-) IDAHO RES FOUND INC.
XX	
PI	Bohach GI;
XX	
DR	WPI; 1999-358008/30.
XX	N-PSDB; AAX58887.
XX	
PT	Non-toxic modified staphylococcal enterotoxins
XX	

PS Claim 16; Page 23; 25pp; English.

XX This sequence represents the mutated disulfide loop region of

CC Staphylococcus aureus group C enterotoxin SECI deletion mutant

CC SECI-12. Amino acids 95-106 in the disulfide loop region of

CC native SECI (see AAY06249) are deleted in SECI-12, and the residue

CC corresponding to native Tyr-94 is changed to Cys. The invention

CC relates to pyrogenic toxins, such as staphylococcal enterotoxins,

CC that are modified in the disulfide loop. Typically, the

CC modification involves deletions within the disulfide loop region

CC of SECI (see AAY06259-61). The modified toxins retain useful

CC biological properties, such as the ability to induce cytokine

CC production, but have substantially reduced toxicity compared to

CC the corresponding unmodified native toxin. Emetic response

CC inducing activity and fever inducing activity are typically

CC decreased by at least about 100-fold, while ID50 (in Dutch Belted

CC rabbits) is at least 100-fold higher than the native toxin.

XX

Sequence 6 AA;

Query Match 100.0%; Score 43; DB 20; Length 6;

Best Local Similarity 100.0%; Pred. No. 7.8e+05;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CCGKTC 6

DB 1 CCGKTC 6

RESULT 2

ABB66318

ID ABB66318 standard; Protein; 779 AA.

XX

AC ABB66318;

XX

26-MAR-2002 (first entry)

DE Drosophila melanogaster polypeptide SEQ ID NO 25746.

XX

KM Drosophila: developmental biology; cell signalling; insecticide;

XX

OS Pharmaceutical.

XX

OS Drosophila melanogaster.

XX

PN WO200171042-A2.

XX

27-SEP-2001.

PD

XX

23-MAR-2001; 2001WO-US09231.

PF

XX

23-MAR-2000; 2000US-191637P.

PR

XX

11-JUL-2000; 2000US-0614150.

PR

XX

PA (PEKE) PE CORP NY.

XX

PI Venter JC, Adams M, Li PWD, Myers EW;

XX

WPI; 2001-656860/75.

DR

XX

N-PSDB; ABL10421.

DR

XX

New isolated nucleic acid detection reagent for detecting 1000 or more

PT genes from Drosophila and for elucidating cell signalling and cell-cell

PT interactions -

XX

PS Disclosure; SEQ ID NO 25746; 21pp + Sequence Listing; English.

XX

The invention relates to an isolated nucleic acid detection reagent

CC capable of detecting 1000 or more genes from Drosophila. The invention is

CC useful in developmental biology and in elucidating cell signalling and

CC cell-cell interactions in higher eukaryotes for the development of

CC insecticides, therapeutics and pharmaceutical drugs. The invention

CC discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA

CC sequences (ABL01840-ABL16175) and the encoded proteins

CC (ABB57737-ABB72072).

CC The sequence data for this patent did not form part of the printed

CC specification, but was obtained in electronic format directly from WIPO

CC at ftp.wipo.int/pub/published_pct_sequences.

XX

Sequence 779 AA;

Query Match 90.7%; Score 39; DB 22; Length 779;

Best Local Similarity 83.3%; Pred. No. 5.3e+02;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 CCGKTC 6

DB 340 CCGKTC 345

RESULT 3

ABB09028

ID ABB09028 standard; peptide; 33 AA.

XX

AC ABB09028;

XX

03-MAY-2002 (first entry)

DE Imperatoxin linear peptide #16.

XX

KM Imperatoxin; muscle disorder.

XX

OS Unidentified.

XX

PN KR2001070886-A.

XX

27-JUL-2001.

PD

XX

18-JUN-2001; 2001KR-0034219.

PF

XX

18-JUN-2001; 2001KR-0034219.

PR

XX

PA (ANYG-) ANYGEN CO LTD.

XX

PA (KMAN-) KMANJU INST SCI & TECHNOLOGY.

XX

PI Kim DH, Kim JI, Lee CW;

XX

WPI; 2002-081143/11.

DR

XX

Three dimensional structure of peptide Imperatoxin and its

PT physiologically active region and manufacturing method -

XX

PS Disclosure; Fig 4; 19pp; Korean.

XX

This invention relates to manufacturing Imperatoxin peptides in a high

CC yield and developing Imperatoxin in a three dimensional structure

CC which is useful in developing medications against muscle disorders.

CC This peptide sequence represents a linear Imperatoxin peptide.

XX

Sequence 33 AA;

Query Match 88.4%; Score 38; DB 23; Length 33;

Best Local Similarity 83.3%; Pred. No. 73;

Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 CCGKTC 6

DB 16 CCGKTC 21

RESULT 4

AAV50923

ID AAV50923 standard; Protein; 232 AA.

XX

AC AAV50923;

XX

10-MAR-2000 (first entry)

DE XX Human fetal brain cDNA clone vc10_1 derived protein.
 XX
 KW Human; secreted protein; treatment; nutritional activity; cytokine;
 KW cell proliferation; cell differentiation; hematopoiesis regulation;
 KW tissue growth; activin; inhibin; chemotactic; chemokinetic; hemostatic;
 KW thrombolytic; anti-inflammatory; invasion suppressor; tumor inhibition;
 KW gene therapy.
 OS Homo sapiens.
 XX
 PN W09955721-A1.
 XX
 PD 04-NOV-1999.
 XX
 PF 23-APR-1999; 99MO-US08504.
 XX
 PR 24-APR-1998; 98US-0082904.
 PR 11-JUN-1998; 98US-0088994.
 PR 12-JUN-1998; 98US-0089278.
 PR 02-JUL-1998; 98US-0091647.
 PR 24-AUG-1998; 98US-0097639.
 PR 22-APR-1999; 99US-0097639.
 XX
 PA (ALPH-) ALPHAGENE INC.
 XX
 PI Valenzuela D, Yuan O, Hoffman H, Hall J, Rapleyko P;
 XX
 DR WPI: 2000-052801/04.
 DR N-PSDB; AA243790.
 XX
 PT New polynucleotides encoding secreted human proteins, derived from
 PT human fetal brain, adult skin, adult brain, adult heart, adult thymus
 PT and adult aorta cDNA libraries.
 XX
 PS Claim 37a; Page 235-236; 282pp; English.
 XX
 CC This invention describes novel human secreted proteins which are encoded
 CC by polynucleotides obtained from fetal brain, adult skin, adult brain,
 CC adult heart, adult thymus and adult aorta cDNA libraries. The
 CC polynucleotides and proteins are predicted to have biological activities
 CC which would make them suitable for treating, preventing or ameliorating
 CC medical conditions in humans and animals, although no supporting data
 CC is given. Suggested activities include nutritional activity, cytokine
 CC and cell proliferation/differentiation activity, immune stimulating
 CC (e.g. as vaccines) or suppressing activity, hematopoiesis regulating
 CC activity, tissue growth activity, activin/inhibin activity,
 CC chemotactic/chemokinetic activity, hemostatic and thrombolytic activity,
 CC receptor/ligand activity, anti-inflammatory activity, cadherin/tumor
 CC invasion suppressor activity, and tumor inhibition activity.
 CC polynucleotides are also stated to be useful for gene therapy.
 CC AA55905-Y50947 represent the secreted proteins described in the method
 CC of the invention which are encoded by the polynucleotides represented in
 CC AA243777-243808.
 CC
 SQ Sequence 232 AA;
 QY 1 CCGATC 6
 DB 70 CCGGTC 75
 DB
 Query Match 88.4%; Score 38; DB 21; Length 232;
 Best Local Similarity 83.3%; Pred. No. 3e+02;
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 RESULT 5
 ABB96741
 ID ABB96741 standard; Peptide: 27 AA.
 AC ABB96741;
 XX
 XX 12-JUL-2002 (first entry)

DE XX Omega-conopeptide E6.2 generic toxin sequence.
 XX
 KW Omega-conopeptide; analgesic; anticonvulsant; vasotropic; cardiant;
 KW neuroprotective; cerebroprotective; cardiovascular; antiinflammatory;
 KW antinigraine; antidiabetic; tranquilizer; vulnary; antipsychotic;
 KW antilytic; neuroleptic; voltage gated ion channel; seizure; epilepsy;
 KW neurological disorder; neurotoxic injury; hypoxia; anoxia; ischaemia;
 KW stroke; cerebrovascular accident; brain trauma; spinal chord trauma;
 KW drowning; suffocation; perinatal asphyxia; hypoglycaemic event; pain;
 KW migraine; inflammation; cardiovascular disorder; psychiatric disorder;
 KW psychosis; anxiety; schizophrenia.
 XX
 OS Conus ermineus.
 XX
 FH Key location/Qualifiers
 FT MISC-difference 1 /label- OTHER
 FT /note- OTHER is Pro or Hydroxy Pro"
 FT MISC-difference 4 /label- OTHER
 FT /note- OTHER is Pro or Hydroxy Pro"
 FT MISC-difference 11 /label- OTHER
 FT /note- OTHER is Pro or Hydroxy Pro"
 FT MISC-difference 27 /label- OTHER
 FT /note- OTHER is Pro or Hydroxy Pro"
 FT MISC-difference 27 /label- OTHER
 FT /note- OTHER is Pro or Hydroxy Pro"
 XX
 PN W0200207675-A2.
 XX
 PD 31-JAN-2002.
 XX
 PE 23-JUL-2001; 2001WO-US23041.
 XX
 PR 21-JUL-2000; 2000US-219616P.
 PR 05-FEB-2001; 2001US-265888P.
 XX
 PA (UTAH) UNIV UTAH RES FOUND.
 PA (COGN-) COGNETIX INC.
 XX
 PI Olivera BM, McIntosh JM, Watkins M, Garrett JE, Shon K;
 PI Jacobsen R, Jones RM, Cartier GE;
 XX
 DR WPI: 2002-257318/30.
 XX
 PT New omega-conopeptides useful for treating disorders associated with
 PT voltage gated ion channels e.g. pain, inflammation, neurological or
 PT cardiovascular disorders -
 XX
 PS Example 2; Page 42; 195pp; English.
 XX
 CC The invention relates to isolated omega-conopeptides, nucleic acid
 CC sequences encoding them, and propeptide sequences. The activity of
 CC the peptides of the invention may be described as, analgesic,
 CC anticonvulsant, vasotropic, cardiant, neuroprotective, cerebroprotective,
 CC cardiovascular, antiinflammatory, antinigraine, antidiabetic,
 CC tranquilizer, vulnary, antipsychotic, anxiolytic and neuroleptic.
 CC peptides of the invention act by modulating the activity of voltage gated
 CC ion channels. They may be used for treating or preventing disorders
 CC associated with voltage gated ion channels such as neurological
 CC disorders, e.g. seizure (associated with epilepsy), neurotoxic injury
 CC associated with conditions of hypoxia, anoxia, ischaemia, stroke,
 CC cerebrovascular accident, brain or spinal chord trauma, drowning,
 CC suffocation, perinatal asphyxia or hypoglycaemic events; pain e.g.
 CC migraine; inflammation or cardiovascular disorders. They may also be used
 CC for treating psychiatric disorders e.g. psychosis, anxiety or
 CC schizophrenia. The analgesic agents of the invention show diminished side
 CC effects and toxicity, and are non-addictive. The sequences given in
 CC records ABB96698-ABB96806 represent omega-conopeptide generic toxin
 CC sequences.
 XX
 SQ Sequence 27 AA;

Query Match 86.0%; Score 37; DB 23; Length 27;
 Best Local Similarity 83.3%; Pred. No. 86;
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 CCGKTC 6
 11111
 DB 16 CCKNKC 21

RESULT 6

ABB96846
 ID ABB96846 standard; peptide; 27 AA.

AC ABB96846;
 DT 12-JUL-2002 (first entry)
 DE Omega-conopeptide E6.2 toxin sequence.

XX Omega-conopeptide; analgesic; anticonvulsant; vasotropic; cardiant;
 KW neuroprotective; cerebroprotective; cardiovascular; antiinflammatory;
 KW antimigraine; antidiabetic; tranquiliser; vulnerary; antipsychotic;
 KW anxiolytic; neuroleptic; voltage gated ion channel; seizure; epilepsy;
 KW neurological disorder; neurotoxic injury; hypoxia; anoxia; ischaemia;
 KW stroke; cerebrovascular accident; brain trauma; spinal chord trauma;
 KW drowning; suffocation; perinatal asphyxia; hypoglycaemic event; pain;
 KW migraine; inflammation; cardiovascular disorder; psychiatric disorder;
 KW psychosis; anxiety; schizophrenia.

OS Conus ermineus.

XX WO200207675-A2.

XX 31-JAN-2002.

XX 23-JUL-2001; 2001WO-US23041.

XX 21-JUL-2000; 2000US-219616P.

XX 05-FEB-2001; 2001US-265888P.

XX (UTAH) UNIV UTAH RES FOUND.

XX (COGN-) COGNEXIT INC.

XX Olivera BM, McIntosh JM, Watkins M, Garrett JE, Shon K;
 PI Jacobsen R, Jones RM, Cartier GE;

XX WPI; 2002-257318/30.

DR New omega-conopeptides useful for treating disorders associated with
 XX voltage gated ion channels e.g. pain, inflammation, neurological or
 XX cardiovascular disorders -
 PS Claim 1(a): Page 71; 195pp; English.

XX The invention relates to isolated omega-conopeptides, nucleic acid
 CC sequences encoding them, and propeptide sequences. The activity of
 CC the peptides of the invention may be described as, analgesic,
 CC anticonvulsant, vasotropic, cardiant, neuroprotective, cerebroprotective,
 CC cardiovascular, antiinflammatory, antimigraine, antidiabetic,
 CC tranquiliser, vulnerary, antipsychotic, anxiolytic and neuroleptic.
 CC Peptides of the invention act by modulating the activity of voltage gated
 CC ion channels. They may be used for treating or preventing disorders
 CC associated with voltage gated ion channels such as neurological
 CC disorders, e.g. seizure (associated with epilepsy), neurotoxic injury
 CC associated with conditions of hypoxia, anoxia, ischaemia, stroke,
 CC cerebrovascular accident, brain or spinal chord trauma, drowning,
 CC suffocation, perinatal asphyxia or hypoglycaemic events; pain e.g.
 CC migraine; inflammation or cardiovascular disorders. They may also be used
 CC for treating psychiatric disorders e.g. psychosis, anxiety or
 CC schizophrenia. The analgesic agents of the invention show diminished side
 CC effects and toxicity, and are non-addictive. The sequences given in
 CC records ABB96807-ABB96905 represent omega-conopeptide toxin sequences.

XX SQ Sequence 27 AA;

Query Match 86.0%; Score 37; DB 23; Length 27;
 Best Local Similarity 83.3%; Pred. No. 86;
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 CCGKTC 6
 11111
 DB 16 CCKNKC 21

XX 1 CCGKTC 6
 11111
 DB 16 CCKNKC 21

RESULT 7

ABB09013
 ID ABB09013 standard; peptide; 33 AA.

AC ABB09013;

DT 03-MAY-2002 (first entry)

DE Imperatoxin linear peptide #1.

XX Imperatoxin; muscle disorder.

XX Unidentified.

OS KR2001070886-A.

XX 27-JUL-2001.

XX 18-JUN-2001; 2001KR-0034219.

XX 18-JUN-2001; 2001KR-0034219.

XX (ANYG-) ANYGEN CO LTD.

XX (KMAN-) KWANGSU INST SCI & TECHNOLOGY.

XX Kim DH, Kim JI, Lee CW;

XX WPI; 2002-081143/11.

XX Three dimensional structure of peptide imperatoxin and its
 PT physiologically active region and manufacturing method -
 XX Disclosure; Fig 4; 19pp; Korean.

XX This invention relates to manufacturing imperatoxin peptides in a high
 CC yield and developing imperatoxin in a three dimensional structure
 CC which is useful in developing medications against muscle disorders.
 CC This peptide sequence represents a linear imperatoxin peptide.

XX Sequence 33 AA;

Query Match 86.0%; Score 37; DB 23; Length 33;
 Best Local Similarity 83.3%; Pred. No. 99;
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCGKTC 6
 11111
 DB 16 CCGKTC 21

RESULT 8

ABB09014
 ID ABB09014 standard; peptide; 33 AA.

AC ABB09014;

DT 03-MAY-2002 (first entry)

DE Imperatoxin linear peptide #2.

XX Imperatoxin; muscle disorder.

XX Unidentified.
OS
XX KR2001070886-A.
PN
XX
PD 27-JUL-2001.
XX
PF 18-JUN-2001; 2001KR-0034219.
XX
PR 18-JUN-2001; 2001KR-0034219.
XX
PA (ANYG-) ANYGEN CO LTD.
PI (KMAN-) KWANGJU INST SCI & TECHNOLOGY.
XX
PI Kim DH, Kim JI, Lee CW;
XX
DR WPI; 2002-081143/11.
XX
PT Three dimensional structure of peptide imperatoxin and its
physiologically active region and manufacturing method -
XX
PS Disclosure; Fig 4; 19pp; Korean.
XX
CC This invention relates to manufacturing imperatoxin peptides in a high
yield and developing imperatoxin in a three dimensional structure
CC which is useful in developing medications against muscle disorders.
CC This peptide sequence represents a linear imperatoxin peptide.
XX
SQ Sequence 33 AA;
SO
Query Match 86.0%; Score 37; DB 23; Length 33;
Best Local Similarity 83.3%; Pred. No. 99;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OY 1 CCGKTC 6
DB 16 CCGKTC 21
RESULT 9
ABB09015
ID ABB09015 standard; peptide; 33 AA.
AC ABB09015;
XX
DT 03-MAY-2002 (first entry)
XX
DE Imperatoxin linear peptide #3.
XX
KW Imperatoxin; muscle disorder.
XX
OS Unidentified.
XX
PN KR2001070886-A.
XX
PD 27-JUL-2001.
XX
PF 18-JUN-2001; 2001KR-0034219.
XX
PR 18-JUN-2001; 2001KR-0034219.
XX
PA (ANYG-) ANYGEN CO LTD.
PI (KMAN-) KWANGJU INST SCI & TECHNOLOGY.
XX
PI Kim DH, Kim JI, Lee CW;
XX
DR WPI; 2002-081143/11.
XX
PT Three dimensional structure of peptide imperatoxin and its
physiologically active region and manufacturing method -
XX
PS Disclosure; Fig 4; 19pp; Korean.
XX

CC This invention relates to manufacturing imperatoxin peptides in a high
yield and developing imperatoxin in a three dimensional structure
CC which is useful in developing medications against muscle disorders.
CC This peptide sequence represents a linear imperatoxin peptide.
XX
SQ Sequence 33 AA;
SO
Query Match 86.0%; Score 37; DB 23; Length 33;
Best Local Similarity 83.3%; Pred. No. 99;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OY 1 CCGKTC 6
DB 16 CCGKTC 21
RESULT 10
ABB09016
ID ABB09016 standard; peptide; 33 AA.
AC ABB09016;
XX
DT 03-MAY-2002 (first entry)
XX
DE Imperatoxin linear peptide #4.
XX
KW Imperatoxin; muscle disorder.
XX
OS Unidentified.
XX
PN KR2001070886-A.
XX
PD 27-JUL-2001.
XX
PF 18-JUN-2001; 2001KR-0034219.
XX
PR 18-JUN-2001; 2001KR-0034219.
XX
PA (ANYG-) ANYGEN CO LTD.
PI (KMAN-) KWANGJU INST SCI & TECHNOLOGY.
XX
PI Kim DH, Kim JI, Lee CW;
XX
DR WPI; 2002-081143/11.
XX
DE Three dimensional structure of peptide imperatoxin and its
physiologically active region and manufacturing method -
XX
PS Disclosure; Fig 4; 19pp; Korean.
XX
OS This invention relates to manufacturing imperatoxin peptides in a high
yield and developing imperatoxin in a three dimensional structure
CC which is useful in developing medications against muscle disorders.
CC This peptide sequence represents a linear imperatoxin peptide.
XX
SQ Sequence 33 AA;
SO
Query Match 86.0%; Score 37; DB 23; Length 33;
Best Local Similarity 83.3%; Pred. No. 99;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OY 1 CCGKTC 6
DB 16 CCGKTC 21
RESULT 11
ABB09017
ID ABB09017 standard; peptide; 33 AA.
AC ABB09017;
XX
DT 03-MAY-2002 (first entry)
XX

XX Imperatoxin linear peptide #5.
DE
XX
KW Imperatoxin; muscle disorder.
XX
OS Unidentified.
XX
PN KR2001070886-A.
XX
PD 27-JUL-2001.
XX
PF 18-JUN-2001; 2001KR-0034219.
XX
PR 18-JUN-2001; 2001KR-0034219.
XX
PA (ANYG-) ANYGEN CO LTD.
XX (KWAN-) KWANGJU INST SCI & TECHNOLOGY.
PI Kim DH, Kim JI, Lee CW;
XX
DR WPI: 2002-081143/11.
XX
PT Three dimensional structure of peptide Imperatoxin and its physiologically active region and manufacturing method -

PS Disclosure; Fig 4; 19pp; Korean.
XX
CC This invention relates to manufacturing Imperatoxin peptides in a high yield and developing Imperatoxin in a three dimensional structure which is useful in developing medications against muscle disorders.
CC This peptide sequence represents a linear Imperatoxin peptide.
XX
SQ Sequence 33 AA;
Query Match 86.0%; Score 37; DB 23; Length 33;
Best Local Similarity 83.3%; Pred. No. 99;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 CCGKTC 6
 |||||
DB 16 CCGKTC 21

RESULT 12
ABB09018
ID ABB09018 standard; peptide: 33 AA.
XX
AC ABB09018;
XX
DT 03-MAY-2002 (first entry)
XX
DE Imperatoxin linear peptide #6.
XX
KW Imperatoxin; muscle disorder.
XX
OS Unidentified.
XX
PN KR2001070886-A.
XX
PD 27-JUL-2001.
XX
PF 18-JUN-2001; 2001KR-0034219.
XX
PR 18-JUN-2001; 2001KR-0034219.
XX
PA (ANYG-) ANYGEN CO LTD.
XX (KWAN-) KWANGJU INST SCI & TECHNOLOGY.
PI Kim DH, Kim JI, Lee CW;
XX
DR WPI: 2002-081143/11.
XX
PT Three dimensional structure of peptide Imperatoxin and its

PT physiologically active region and manufacturing method -
XX
XX Disclosure; Fig 4; 19pp; Korean.
PS
XX
CC This invention relates to manufacturing Imperatoxin peptides in a high yield and developing Imperatoxin in a three dimensional structure which is useful in developing medications against muscle disorders.
CC This peptide sequence represents a linear Imperatoxin peptide.
XX
SQ Sequence 33 AA;
Query Match 86.0%; Score 37; DB 23; Length 33;
Best Local Similarity 83.3%; Pred. No. 99;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 CCGKTC 6
 |||||
DB 16 CCGKTC 21

RESULT 13
ABB09019
ID ABB09019 standard; peptide: 33 AA.
XX
AC ABB09019;
XX
DT 03-MAY-2002 (first entry)
XX
DE Imperatoxin linear peptide #7.
XX
KW Imperatoxin; muscle disorder.
XX
OS Unidentified.
XX
PN KR2001070886-A.
XX
PD 27-JUL-2001.
XX
PF 18-JUN-2001; 2001KR-0034219.
XX
PR 18-JUN-2001; 2001KR-0034219.
XX
PA (ANYG-) ANYGEN CO LTD.
XX (KWAN-) KWANGJU INST SCI & TECHNOLOGY.
PI Kim DH, Kim JI, Lee CW;
XX
DR WPI: 2002-081143/11.
XX
PT Three dimensional structure of peptide Imperatoxin and its physiologically active region and manufacturing method -

PS Disclosure; Fig 4; 19pp; Korean.
XX
CC This invention relates to manufacturing Imperatoxin peptides in a high yield and developing Imperatoxin in a three dimensional structure which is useful in developing medications against muscle disorders.
CC This peptide sequence represents a linear Imperatoxin peptide.
XX
SQ Sequence 33 AA;
Query Match 86.0%; Score 37; DB 23; Length 33;
Best Local Similarity 83.3%; Pred. No. 99;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 CCGKTC 6
 |||||
DB 16 CCGKTC 21

RESULT 14
ABB09020
ID ABB09020 standard; peptide: 33 AA.
XX
XX

XX ABB09020;
 AC 03-MAY-2002 (first entry)
 DT Imperatoxin linear peptide #8.
 DE Imperatoxin; muscle disorder.
 KW Imperatoxin; muscle disorder.
 OS Unidentified.
 XX KR2001070886-A.
 PN 27-JUL-2001.
 PD 18-JUN-2001; 2001KR-0034219.
 PF 18-JUN-2001; 2001KR-0034219.
 PR 18-JUN-2001; 2001KR-0034219.
 XX (ANYG-) ANYGEN CO LTD.
 PA (KWAN-) KWANGJU INST SCI & TECHNOLOGY.
 XX Kim DH, Kim JI, Lee CW;
 PI WPI; 2002-081143/11.
 DR Three dimensional structure of peptide imperatoxin and its
 XX physiologically active region and manufacturing method -
 XX PS Disclosure; Fig 4; 19pp; Korean.
 CC This invention relates to manufacturing imperatoxin peptides in a high
 CC yield and developing imperatoxin in a three dimensional structure
 CC which is useful in developing medications against muscle disorders.
 CC This peptide sequence represents a linear imperatoxin peptide.
 XX SQ Sequence 33 AA;
 QY Query Match 86.0%; Score 37; DB 23; Length 33;
 Best Local Similarity 83.3%; Pred. No. 99;
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 DB 1 CCGKTC 6
 16 CCGKCC 21
 RESULT 15
 ABB09021
 ID ABB09021 standard; peptide; 33 AA.
 AC ABB09021;
 XX 03-MAY-2002 (first entry)
 DT Imperatoxin linear peptide #9.
 DE Imperatoxin; muscle disorder.
 KW Imperatoxin; muscle disorder.
 OS Unidentified.
 XX KR2001070886-A.
 PN 27-JUL-2001.
 PD 18-JUN-2001; 2001KR-0034219.
 PF 18-JUN-2001; 2001KR-0034219.
 PR 18-JUN-2001; 2001KR-0034219.
 XX (ANYG-) ANYGEN CO LTD.
 PA (KWAN-) KWANGJU INST SCI & TECHNOLOGY.
 XX Kim DH, Kim JI, Lee CW;
 PI

XX WPI; 2002-081143/11.
 DR Three dimensional structure of peptide imperatoxin and its
 XX physiologically active region and manufacturing method -
 XX PS Disclosure; Fig 4; 19pp; Korean.
 CC This invention relates to manufacturing imperatoxin peptides in a high
 CC yield and developing imperatoxin in a three dimensional structure
 CC which is useful in developing medications against muscle disorders.
 CC This peptide sequence represents a linear imperatoxin peptide.
 XX SQ Sequence 33 AA;
 QY Query Match 86.0%; Score 37; DB 23; Length 33;
 Best Local Similarity 83.3%; Pred. No. 99;
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 DB 1 CCGKTC 6
 16 CCGKCC 21

Search completed: May 6, 2003, 10:29:11
 Job time : 37 secs

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GenCore version 5.1.4_p5_4578
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OM protein - protein search, using sw model

Run on: May 6, 2003, 10:28:55 ; Search time 14 seconds
(without alignments)
12.610 Million cell updates/sec

Title: US-09-555-115a-66
Perfect score: 43
Sequence: 1 CCGKTC 6

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: Issued Patents, AA: *

1: /cgn2_6/ptodata/1/1aa/5A.COMB.pep:*
2: /cgn2_6/ptodata/1/1aa/5B.COMB.pep:*
3: /cgn2_6/ptodata/1/1aa/6A.COMB.pep:*
4: /cgn2_6/ptodata/1/1aa/6B.COMB.pep:*
5: /cgn2_6/ptodata/1/1aa/6C.COMB.pep:*
6: /cgn2_6/ptodata/1/1aa/6D.COMB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	37	86.0	1345	2	US-08-977-767-3
2	37	86.0	1400	4	US-08-630-915A-37
3	37	86.0	1417	4	US-08-900-230-3
4	37	86.0	1917	4	US-09-627-650B-5
5	37	86.0	1917	4	US-09-436-063C-5
6	36	83.7	57	4	US-08-900-230-59
7	36	83.7	2088	4	US-09-548-372D-13
8	36	83.7	2088	4	US-09-548-367D-13
9	35	81.4	24	4	US-09-201-227A-34
10	35	81.4	38	2	US-08-902-516-47
11	35	81.4	111	4	US-09-201-227A-39
12	35	81.4	2211	4	US-09-738-884-1
13	34	79.1	124	4	US-09-201-227A-37
14	34	79.1	154	4	US-09-201-227A-4
15	34	79.1	154	4	US-09-201-227A-18
16	34	79.1	193	3	US-08-842-976-3
17	34	79.1	193	3	US-08-842-976-4
18	34	79.1	193	3	US-09-213-397-3
19	34	79.1	193	3	US-09-213-397-4
20	34	79.1	193	3	US-09-416-489-3
21	34	79.1	193	3	US-09-416-489-4
22	34	79.1	197	1	US-07-914-284A-8
23	34	79.1	198	4	US-08-842-306B-2
24	34	79.1	198	4	US-08-838-973B-2
25	34	79.1	198	4	US-08-771-212A-2
26	34	79.1	202	2	US-08-948-616-11
27	34	79.1	202	2	US-09-193-510-11

28	34	79.1	202	4	US-09-368-402-11	Sequence 11, Appl
29	34	79.1	207	4	US-09-415-522-2	Sequence 2, Appl
30	33	76.7	26	4	US-09-227-357-579	Sequence 579, App
31	33	76.7	30	2	US-08-753-829A-8	Sequence 8, Appl
32	33	76.7	425	1	US-08-414-926A-15	Sequence 15, Appl
33	33	76.7	425	1	US-08-926-922-15	Sequence 15, Appl
34	33	76.7	425	3	US-09-253-682-15	Sequence 15, Appl
35	33	76.7	425	4	US-09-527-657-15	Sequence 15, Appl
36	33	76.7	2296	2	US-08-286-819A-27	Sequence 27, Appl
37	33	76.7	2296	3	US-08-980-357-27	Sequence 27, Appl
38	32	74.4	23	4	US-08-900-230-23	Sequence 23, Appl
39	32	74.4	197	2	US-08-855-261A-1	Sequence 1, Appl
40	32	74.4	197	4	US-09-227-224-1	Sequence 1, Appl
41	32	74.4	198	4	US-09-227-357-232	Sequence 232, App
42	32	74.4	282	3	US-09-120-365-79	Sequence 79, Appl
43	32	74.4	282	4	US-09-515-039-79	Sequence 79, Appl
44	32	74.4	339	1	US-08-208-007A-11	Sequence 11, Appl
45	32	74.4	339	1	US-08-330-121B-7	Sequence 7, Appl

ALIGNMENTS

RESULT 1
US-08-977-767-3
Sequence 3, Application US/08977767
Patent No. 5972684
GENERAL INFORMATION:
APPLICANT: Bandman, Olga
APPLICANT: Yue, Henry
APPLICANT: Greenwald, Sara
APPLICANT: Corley, Neil C.
TITLE OF INVENTION: CARBONIC ANHYDRASE VIII
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/977,767
FILING DATE: Herewith
CLASSIFICATION: 424
PRIOR APPLICATION NUMBER:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0423 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
TELEFAX: 650-845-4166
TELEX:
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1345 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: Genbank
CLONE: 1532042
US-08-977-767-3
Query Match 86.0%; Score 37; DB 2; Length 1345;

Best Local Similarity 83.3%; Pred. No. 4.3e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 CCGKTC 6
||| ||
DB 820 CCGTTC 825

RESULT 2
US-08-630-915A-37

; Sequence 37, Application US/08630915A
; Patent No. 6309820

; GENERAL INFORMATION:

; APPLICANT: SPARKS, Andrew B.

; APPLICANT: HOFFMAN, No. 6309820h

; APPLICANT: KAY, Brian K.

; APPLICANT: FOWLES, Dana M.

; APPLICANT: MCCONNELL, Stephen J.

; TITLE OF INVENTION: POLYPEPTIDES HAVING A FUNCTIONAL

; TITLE OF INVENTION: DOMAIN OF INTEREST AND METHODS OF IDENTIFYING AND

; NUMBER OF SEQUENCES: 227

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Pennie & Edmonds LLP

; STREET: 1155 Avenue of the Americas

; CITY: New York

; STATE: New York

; COUNTRY: USA

; ZIP: 10036-2711

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patentin Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/630,915A

; FILING DATE: 03-APR-1996

; CLASSIFICATION: 536

; ATTORNEY/AGENT INFORMATION:

; NAME: MISTOCK, S. Leslie

; REGISTRATION NUMBER: 18,872

; REFERENCE/DOCKET NUMBER: 1101-174

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (212) 790-9090

; TELEFAX: (212) 869-8864/9741

; TELEX: 66141 PENNIE

; INFORMATION FOR SEQ ID NO: 37:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 1400 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: DNA

; US-08-630-915A-37

Query Match 86.0%; Score 37; DB 4; Length 1400;
Best Local Similarity 83.3%; Pred. No. 4.5e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 CCGKTC 6
||| ||
DB 579 CCGTTC 584

RESULT 3
US-08-900-230-3

; Sequence 3, Application US/08900230

; Patent No. 6329197

; GENERAL INFORMATION:

; APPLICANT: Bard, Jonathan A.

; TITLE OF INVENTION: DNA ENCODING GALANIN GALR3 RECEPTORS AND

; NUMBER OF SEQUENCES: 59

CORRESPONDENCE ADDRESS:

; ADDRESSEE: Cooper & Dunham LLP

; STREET: 1185 Avenue of the Americas

; CITY: New York

; STATE: New York

; COUNTRY: U.S.A.

; ZIP: 11036

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patentin Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/900,230

; FILING DATE: 23-JUL-1997

; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:

; NAME: White, John P.

; REGISTRATION NUMBER: 28,678

; REFERENCE/DOCKET NUMBER: 52241-C/JPW/ADM

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 212-278-0400

; TELEFAX: 212-391-0525

; INFORMATION FOR SEQ ID NO: 3:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 1417 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE:

; HYPOTHETICAL: NO

; ANTI-SENSE: NO

; US-08-900-230-3

Query Match 86.0%; Score 37; DB 4; Length 1417;
Best Local Similarity 83.3%; Pred. No. 4.5e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 CCGKTC 6
||| ||
DB 1327 CCGTTC 1332

RESULT 4
US-09-627-650B-5

; Sequence 5, Application US/09627650B

; Patent No. 6406872

; GENERAL INFORMATION:

; APPLICANT: Hamber, Bruce

; APPLICANT: Jorgensen, Erik

; TITLE OF INVENTION: Nematode Neuromuscular Junction GABA Receptors and

; FILE REFERENCE: 21101.000903

; CURRENT APPLICATION NUMBER: US/09/627,650B

; CURRENT FILING DATE: 2000-07-28

; PRIOR APPLICATION NUMBER: 09/436,063

; PRIOR FILING DATE: 1999-11-08

; PRIOR APPLICATION NUMBER: 60/107,727

; PRIOR FILING DATE: 1998-11-09

; NUMBER OF SEQ ID NOS: 50

; SOFTWARE: Patentin Ver. 2.1

; SEQ ID NO 5

; LENGTH: 1917

; TYPE: PRT

; ORGANISM: Caenorhabditis elegans

; US-09-627-650B-5

Query Match 86.0%; Score 37; DB 4; Length 1917;
Best Local Similarity 83.3%; Pred. No. 5.6e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 CCGKTC 6
||| ||

Db 1389 CCGTTC 1394

RESULT 5

US-09-436-0630-5
Sequence 5, Application US/09436063C
Patent No. 6407210
GENERAL INFORMATION:
APPLICANT: Bamber, Bruce
APPLICANT: Jorgensen, Erik
TITLE OF INVENTION: Nematode Neuromuscular Junction GABA Receptors and
FILE REFERENCE: P-1095corrected
CURRENT APPLICATION NUMBER: US/09/436,063C
CURRENT FILING DATE: 1999-11-08
PRIOR APPLICATION NUMBER: 60/107727
PRIOR FILING DATE: 1998-11-09
NUMBER OF SEQ ID NOS: 18
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 5
LENGTH: 1917
TYPE: PRT
ORGANISM: Caenorhabditis elegans
US-09-436-0630-5

Query Match 86.0%; Score 37; DB 4; Length 1917;
Best Local Similarity 83.3%; Pred. No. 5.6e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCGTTC 6
Db 1389 CCGTTC 1394

RESULT 6

US-08-900-230-59
Sequence 59, Application US/08900230
Patent No. 6329197
GENERAL INFORMATION:
APPLICANT: Baird, Jonathan A.
TITLE OF INVENTION: DNA ENCODING GALANIN GALR3 RECEPTORS AND
TITLE OF INVENTION: USES THEREOF
NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper & Dunham LLP
STREET: 1185 Avenue of The Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 11036

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/900,230
FILING DATE: 23-JUL-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 52241-C/JPW/ADM
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-278-0400
TELEFAX: 212-391-0525

INFORMATION FOR SEQ ID NO: 59:
SEQUENCE CHARACTERISTICS:
LENGTH: 57 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE:

HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-900-230-59

Query Match 83.7%; Score 36; DB 4; Length 57;
Best Local Similarity 83.3%; Pred. No. 60;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCGTTC 6
Db 48 CCGTTC 53

RESULT 7

US-09-548-372D-13
Sequence 13, Application US/09548372D
Patent No. 6420534
GENERAL INFORMATION:
APPLICANT: GURNEY ET AL.
TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND USE
FILE REFERENCE: 29915/62801
CURRENT APPLICATION NUMBER: US/09/548,372D
CURRENT FILING DATE: 2000-04-12
PRIOR APPLICATION NUMBER: US 60/155,493
PRIOR FILING DATE: 1999-09-23
PRIOR APPLICATION NUMBER: US 09/404,133
PRIOR FILING DATE: 1999-09-23
PRIOR APPLICATION NUMBER: PCT/US99/20881
PRIOR FILING DATE: 1999-09-23
PRIOR APPLICATION NUMBER: US 60/101,594
PRIOR FILING DATE: 1998-09-24
NUMBER OF SEQ ID NOS: 73
SOFTWARE: Patentin version 3.1
SEQ ID NO 13
LENGTH: 2088
TYPE: PRT
ORGANISM: Homo sapiens
US-09-548-372D-13

Query Match 83.7%; Score 36; DB 4; Length 2088;
Best Local Similarity 83.3%; Pred. No. 8.1e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCGTTC 6
Db 1353 CCGTTC 1358

RESULT 8

US-09-548-367D-13
Sequence 13, Application US/09548367D
Patent No. 6440698
GENERAL INFORMATION:
APPLICANT: GURNEY ET AL.
TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR AND USE
FILE REFERENCE: 29915/62801
CURRENT APPLICATION NUMBER: US/09/548,367D
CURRENT FILING DATE: 2000-04-12
PRIOR APPLICATION NUMBER: US 60/155,493
PRIOR FILING DATE: 1999-09-23
PRIOR APPLICATION NUMBER: US 09/404,133
PRIOR FILING DATE: 1999-09-23
PRIOR APPLICATION NUMBER: PCT/US99/20881
PRIOR FILING DATE: 1999-09-23
PRIOR APPLICATION NUMBER: US 60/101,594
PRIOR FILING DATE: 1998-09-24
NUMBER OF SEQ ID NOS: 73
SOFTWARE: Patentin version 3.1
SEQ ID NO 13
LENGTH: 2088
TYPE: PRT

ORGANISM: Homo sapiens
US-09-548-367D-13

Query Match
Best Local Similarity 83.7%; Score 36; DB 4; Length 2088;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCGKTC 6
11111
DB 1353 CCGKTC 1358

RESULT 9
US-09-201-227A-34
Sequence 34, Application US/09201227A
Patent No. 6468770
GENERAL INFORMATION:
APPLICANT: Keyes, Linda N.
APPLICANT: Doherty, Stephen K.
APPLICANT: Buchanan, Andrew R.
TITLE OF INVENTION: NUCLEIC ACIDS AND PROTEINS OF D. MELANOGASTER INSULIN-LIKE,
FILE REFERENCE: 7326-066
CURRENT APPLICATION NUMBER: US/09/201,227A
CURRENT FILING DATE: 1998-11-30
NUMBER OF SEQ ID NOS: 45
SOFTWARE: Patent version 3.0
SEQ ID NO 34
LENGTH: 24
TYPE: PRT
ORGANISM: Locust
US-09-201-227A-34

Query Match
Best Local Similarity 81.4%; Score 35; DB 4; Length 24;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCGKTC 6
11111
DB 9 CCGKTC 14

RESULT 10
US-08-902-516-47
Sequence 47, Application US/08902516
Patent No. 5891432
GENERAL INFORMATION:
APPLICANT: Soo Hoo, William
TITLE OF INVENTION: MEMBRANE-BOUND CYTOKINE COMPOSITIONS
TITLE OF INVENTION: COMPRISING GM-CSF AND METHODS OF MODULATING AN IMMUNE
NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
ADDRESSEE: CAMPBELL & FLORES, LLP
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: United States
ZIP: 92121
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/902,516
FILING DATE: 29-JUL-1997
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-IM 2442
TELECOMMUNICATION INFORMATION:

TELEPHONE: (619)535-9001
TELEFAX: (619)535-8949
INFORMATION FOR SEQ ID NO: 47:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-902-516-47

Query Match
Best Local Similarity 81.4%; Score 35; DB 2; Length 38;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCGKTC 6
11111
DB 23 CCGKTC 28

RESULT 11
US-09-201-227A-39
Sequence 39, Application US/09201227A
Patent No. 6468770
GENERAL INFORMATION:
APPLICANT: Keyes, Linda N.
APPLICANT: Doherty, Stephen K.
APPLICANT: Buchanan, Andrew R.
TITLE OF INVENTION: NUCLEIC ACIDS AND PROTEINS OF D. MELANOGASTER INSULIN-LIKE
FILE REFERENCE: 7326-066
CURRENT APPLICATION NUMBER: US/09/201,227A
CURRENT FILING DATE: 1998-11-30
NUMBER OF SEQ ID NOS: 45
SOFTWARE: Patent version 3.0
SEQ ID NO 39
LENGTH: 111
TYPE: PRT
ORGANISM: Locust
FEATURE:
NAME/KEY: SITE
LOCATION: 34...85
OTHER INFORMATION: Xaa - any amino acid
US-09-201-227A-39

Query Match
Best Local Similarity 81.4%; Score 35; DB 4; Length 111;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCGKTC 6
11111
DB 96 CCGKTC 101

RESULT 12
US-09-738-884-1
Sequence 1, Application US/09738884
Patent No. 6391606
GENERAL INFORMATION:
APPLICANT: GUEGLER, Karl et al
TITLE OF INVENTION: ISOLATED HUMAN PHOSPHOLIPASE PROTEINS,
TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN PHOSPHOLIPASE
FILE REFERENCE: C1000849
CURRENT APPLICATION NUMBER: US/09/738,884
CURRENT FILING DATE: 2000-12-18
NUMBER OF SEQ ID NOS: 5
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 1
LENGTH: 2211
TYPE: PRT
ORGANISM: Human
US-09-738-884-1

Query Match 81.4%; Score 35; DB 4; Length 2211;
 Best Local Similarity 83.3%; Pred. No. 1.1e+03;
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 CCGKTC 6
 DB 63 CCGKTC 68

RESULT 13
 US-09-201-227A-37
 ; Sequence 37, Application US/09201227A
 ; Patent No. 6468770
 ; GENERAL INFORMATION:
 ; APPLICANT: Keyes, Linda N.
 ; APPLICANT: Dobberstein, Stephen K.
 ; APPLICANT: Buchman, Andrew R.
 ; TITLE OF INVENTION: NUCLEIC ACIDS AND PROTEINS OF D. MELANOGASTER INSULIN-LIKE
 ; FILE REFERENCE: 7326-066
 ; CURRENT APPLICATION NUMBER: US/09/201,227A
 ; CURRENT FILING DATE: 1998-11-30
 ; NUMBER OF SEQ ID NOS: 45
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO 37
 ; LENGTH: 124
 ; TYPE: PRT
 ; ORGANISM: Drosophila sp.
 ; FEATURE:
 ; NAME/KEY: SITE
 ; LOCATION: 43... 92
 ; OTHER INFORMATION: Xaa - any amino acid
 US-09-201-227A-37

Query Match 79.1%; Score 34; DB 4; Length 124;
 Best Local Similarity 83.3%; Pred. No. 1.9e+02;
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 CCGKTC 6
 DB 107 CCGKTC 112

RESULT 14
 US-09-201-227A-4
 ; Sequence 4, Application US/09201227A
 ; Patent No. 6468770
 ; GENERAL INFORMATION:
 ; APPLICANT: Keyes, Linda N.
 ; APPLICANT: Dobberstein, Stephen K.
 ; APPLICANT: Buchman, Andrew R.
 ; TITLE OF INVENTION: NUCLEIC ACIDS AND PROTEINS OF D. MELANOGASTER INSULIN-LIKE
 ; FILE REFERENCE: 7326-066
 ; CURRENT APPLICATION NUMBER: US/09/201,227A
 ; CURRENT FILING DATE: 1998-11-30
 ; NUMBER OF SEQ ID NOS: 45
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO 4
 ; LENGTH: 154
 ; TYPE: PRT
 ; ORGANISM: Drosophila melanogaster
 US-09-201-227A-4

Query Match 79.1%; Score 34; DB 4; Length 154;
 Best Local Similarity 83.3%; Pred. No. 2.3e+02;
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 CCGKTC 6
 DB 137 CCGKTC 142

RESULT 15
 US-09-201-227A-18
 ; Sequence 18, Application US/09201227A
 ; Patent No. 6468770
 ; GENERAL INFORMATION:
 ; APPLICANT: Keyes, Linda N.
 ; APPLICANT: Dobberstein, Stephen K.
 ; APPLICANT: Buchman, Andrew R.
 ; TITLE OF INVENTION: NUCLEIC ACIDS AND PROTEINS OF D. MELANOGASTER INSULIN-LIKE
 ; FILE REFERENCE: 7326-066
 ; CURRENT APPLICATION NUMBER: US/09/201,227A
 ; CURRENT FILING DATE: 1998-11-30
 ; NUMBER OF SEQ ID NOS: 45
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO 18
 ; LENGTH: 154
 ; TYPE: PRT
 ; ORGANISM: Drosophila melanogaster
 US-09-201-227A-18

Query Match 79.1%; Score 34; DB 4; Length 154;
 Best Local Similarity 83.3%; Pred. No. 2.3e+02;
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 CCGKTC 6
 DB 137 CCGKTC 142

Search completed: May 6, 2003, 10:32:13
 Job time : 16 secs

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GenCore version 5.1.4_p5-4578
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OM protein - protein search, using sw model

Run on: May 6, 2003, 10:31:11 ; Search time 16 seconds
(without alignments)
32.358 Million cell updates/sec

Title: US-09-555-115a-66

Perfect score: 43

Sequence: 1 CCGKTC 6

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Gapop 10.0 , Gapext 0.5

Searched: 328255 seqs, 86286685 residues

Total number of hits satisfying chosen parameters: 328255

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Published Applications AA.*
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9: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
10: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep.*
11: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
12: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep.*
13: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
14: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	37	86.0	103	9	US-09-984-271-158 Sequence 158, App
2	37	86.0	434	9	US-10-123-155-439 Sequence 439, App
3	37	86.0	584	9	US-10-123-155-401 Sequence 401, App
4	37	86.0	636	9	US-10-184-644-199 Sequence 199, App
5	37	86.0	636	9	US-10-184-634-199 Sequence 199, App
6	37	86.0	744	9	US-10-184-644-255 Sequence 255, App
7	37	86.0	744	9	US-10-184-634-255 Sequence 255, App
8	37	86.0	756	9	US-10-184-644-125 Sequence 125, App
9	37	86.0	756	9	US-10-184-634-125 Sequence 125, App
10	37	86.0	997	9	US-10-184-634-23 Sequence 23, App
11	37	86.0	997	9	US-10-184-644-23 Sequence 23, App
12	37	86.0	1024	9	US-10-123-155-315 Sequence 315, App
13	37	86.0	1047	9	US-10-184-644-447 Sequence 447, App
14	37	86.0	1047	9	US-10-184-634-447 Sequence 447, App
15	37	86.0	1094	9	US-10-184-634-387 Sequence 387, App
16	37	86.0	1094	9	US-10-184-644-387 Sequence 387, App
17	37	86.0	1121	9	US-10-123-155-23 Sequence 23, App
18	37	86.0	1174	9	US-10-184-644-353 Sequence 353, App
19	37	86.0	1174	9	US-10-184-634-353 Sequence 353, App

20	37	86.0	1177	9	US-10-184-644-381 Sequence 381, App
21	37	86.0	1177	9	US-10-184-634-381 Sequence 381, App
22	37	86.0	1220	9	US-10-184-644-557 Sequence 557, App
23	37	86.0	1220	9	US-10-184-634-557 Sequence 557, App
24	37	86.0	1231	9	US-10-123-155-279 Sequence 279, App
25	37	86.0	1234	9	US-10-184-644-237 Sequence 237, App
26	37	86.0	1234	9	US-10-184-634-237 Sequence 237, App
27	37	86.0	1248	9	US-10-184-644-587 Sequence 587, App
28	37	86.0	1248	9	US-10-184-634-587 Sequence 587, App
29	37	86.0	1281	9	US-10-123-155-509 Sequence 509, App
30	37	86.0	1300	9	US-10-174-590-269 Sequence 269, App
31	37	86.0	1300	9	US-10-176-738-269 Sequence 269, App
32	37	86.0	1300	9	US-10-175-737-269 Sequence 269, App
33	37	86.0	1300	9	US-10-173-706-269 Sequence 269, App
34	37	86.0	1300	9	US-10-175-738-269 Sequence 269, App
35	37	86.0	1300	9	US-10-175-752-269 Sequence 269, App
36	37	86.0	1300	9	US-10-176-482-269 Sequence 269, App
37	37	86.0	1300	9	US-10-176-757-269 Sequence 269, App
38	37	86.0	1300	9	US-10-176-913-269 Sequence 269, App
39	37	86.0	1300	9	US-10-180-552-269 Sequence 269, App
40	37	86.0	1300	9	US-10-180-557-269 Sequence 269, App
41	37	86.0	1300	9	US-10-173-700-269 Sequence 269, App
42	37	86.0	1300	9	US-10-174-572-269 Sequence 269, App
43	37	86.0	1300	9	US-10-174-579-269 Sequence 269, App
44	37	86.0	1300	9	US-10-174-582-269 Sequence 269, App
45	37	86.0	1300	9	US-10-174-588-269 Sequence 269, App

ALIGNMENTS

RESULT 1
US-09-984-271-158
Sequence 158, Application US/09984271
Publication No. US20030040088A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: P2030P1
FILE REFERENCE: P2030P1
CURRENT APPLICATION NUMBER: US/09/984, 271
CURRENT FILING DATE: 2001-10-29
PRIOR APPLICATION NUMBER: 09/482, 273
PRIOR FILING DATE: 2000-01-13
PRIOR APPLICATION NUMBER: PCT/US99/15849
PRIOR FILING DATE: 1999-07-14
PRIOR APPLICATION NUMBER: 60/092, 921
PRIOR FILING DATE: 1998-07-15
PRIOR APPLICATION NUMBER: 60/092, 922
PRIOR FILING DATE: 1998-07-15
PRIOR APPLICATION NUMBER: 60/092, 956
PRIOR FILING DATE: 1998-07-15
NUMBER OF SEQ ID NOS: 267
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 158
LENGTH: 103
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: SITE
LOCATION: (103)
OTHER INFORMATION: Xaa equals stop translation
US-09-984-271-158

Query Match: 86.0%; Score 37; DB 9; Length 103;
Best Local Similarity: 83.3%; Pred. No. 83;
Matches: 5; Conservative: 0; Mismatches: 1; Indels: 0; Gaps: 0;

QY 1 CCGKTC 6
DB 38 CCGKTC 43

RESULT 2

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US-10-123-155-439
; Sequence 439, Application US/10123155
; Publication No. US20030068794A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tamas, Daniel
; APPLICANT: Watanabe, Collin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C30
; CURRENT APPLICATION NUMBER: US/10/123,155
; PRIOR APPLICATION REMOVED - See Palm or File Wrapper
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 439
; LENGTH: 434
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-123-155-439

Query Match      86.0%; Score 37; DB 9; Length 434;
Best Local Similarity 83.3%; Pred. No. 2.6e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCGKTC 6
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Db 251 CCGATC 256

RESULT 3
US-10-123-155-401
; Sequence 401, Application US/10123155
; Publication No. US20030068794A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tamas, Daniel
; APPLICANT: Watanabe, Collin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C30
; CURRENT APPLICATION NUMBER: US/10/123,155
; PRIOR APPLICATION REMOVED - See Palm or File Wrapper
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 401
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; LENGTH: 584
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-123-155-401

Query Match      86.0%; Score 37; DB 9; Length 584;
Best Local Similarity 83.3%; Pred. No. 3.2e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCGKTC 6
    ||| ||
Db 331 CCGATC 336

RESULT 4
US-10-184-644-199
; Sequence 199, Application US/10184644
; Publication No. US20030044930A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Collin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3430R1C227
; CURRENT APPLICATION NUMBER: US/10/184,644
; CURRENT FILING DATE: 2002-06-28
; PRIOR APPLICATION REMOVED - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 199
; LENGTH: 636
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-184-644-199

Query Match      86.0%; Score 37; DB 9; Length 636;
Best Local Similarity 83.3%; Pred. No. 3.5e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCGKTC 6
    ||| ||
Db 3 CCGTTC 8

RESULT 5
US-10-184-634-199
; Sequence 199, Application US/10184634
; Publication No. US20030068684A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Collin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3430R1C217
; CURRENT APPLICATION NUMBER: US/10/184,634
; CURRENT FILING DATE: 2002-06-28
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; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 199
; LENGTH: 636
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-184-634-199

Query Match
Best Local Similarity 86.0%; Score 37; DB 9; Length 636;
Pred. No. 3.5e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 CCGKTC 6
||| ||
Db 3 CCGTTC 8

RESULT 6
US-10-184-644-255

; Sequence 255, Application US/10184644
; Publication No. US20030044930A1
; GENERAL INFORMATION:

; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3430R1C227
; CURRENT APPLICATION NUMBER: US/10/184,644
; CURRENT FILING DATE: 2002-06-28
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 255
; LENGTH: 744
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-184-644-255

Query Match
Best Local Similarity 86.0%; Score 37; DB 9; Length 744;
Pred. No. 3.9e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 CCGKTC 6
||| ||
Db 205 CCGTTC 210

RESULT 7
US-10-184-634-255

; Sequence 255, Application US/10184634
; Publication No. US20030068684A1
; GENERAL INFORMATION:

; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME

; FILE REFERENCE: P3430R1C217
; CURRENT APPLICATION NUMBER: US/10/184,634
; CURRENT FILING DATE: 2002-06-28
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 255
; LENGTH: 744
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-184-634-255

Query Match
Best Local Similarity 86.0%; Score 37; DB 9; Length 744;
Pred. No. 3.9e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 CCGKTC 6
||| ||
Db 205 CCGTTC 210

RESULT 8
US-10-184-644-125

; Sequence 125, Application US/10184644
; Publication No. US20030044930A1
; GENERAL INFORMATION:

; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3430R1C227
; CURRENT APPLICATION NUMBER: US/10/184,644
; CURRENT FILING DATE: 2002-06-28
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 125
; LENGTH: 756
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-184-644-125

Query Match
Best Local Similarity 86.0%; Score 37; DB 9; Length 756;
Pred. No. 4e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 CCGKTC 6
||| ||
Db 538 CCGATC 543

RESULT 9
US-10-184-634-125

; Sequence 125, Application US/10184634
; Publication No. US20030068684A1
; GENERAL INFORMATION:

; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.

```

; APPLICANT: Zhang,Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3430R1C217
; CURRENT APPLICATION NUMBER: US/10/184,634
; CURRENT FILING DATE: 2002-06-28
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 125
; LENGTH: 756
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-184-634-125

Query Match
Best Local Similarity 86.0%; Score 37; DB 9; Length 756;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCGKTC 6
DB 538 CCGATC 543

RESULT 10
US-10-184-644-23
; Sequence 23, Application US/10184644
; Publication No. US20030044930A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3430R1C227
; CURRENT APPLICATION NUMBER: US/10/184,644
; CURRENT FILING DATE: 2002-06-28
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 23
; LENGTH: 997
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-184-644-23

Query Match
Best Local Similarity 86.0%; Score 37; DB 9; Length 997;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCGKTC 6
DB 10 CCGATC 15

RESULT 11
US-10-184-634-23
; Sequence 23, Application US/10184634
; Publication No. US20030068684A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
```

```

; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3430R1C217
; CURRENT APPLICATION NUMBER: US/10/184,634
; CURRENT FILING DATE: 2002-06-28
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 23
; LENGTH: 997
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-184-634-23

Query Match
Best Local Similarity 86.0%; Score 37; DB 9; Length 997;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCGKTC 6
DB 10 CCGATC 15

RESULT 12
US-10-123-155-315
; Sequence 315, Application US/10123155
; Publication No. US20030068794A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3330R1C30
; CURRENT APPLICATION NUMBER: US/10/123,155
; CURRENT FILING DATE: 2002-04-15
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 315
; LENGTH: 1024
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-123-155-315

Query Match
Best Local Similarity 86.0%; Score 37; DB 9; Length 1024;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCGKTC 6
DB 776 CCGATC 781

RESULT 13
US-10-184-644-447
; Sequence 447, Application US/10184644
```

```
Publication NO. US20030044930A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Chen, Jian
APPLICANT: Desnoyers, Luc
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Pan, James
APPLICANT: Smith, Victoria
APPLICANT: Watanabe, Collin K.
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P3430R1C227
CURRENT APPLICATION NUMBER: US/10/184,644
CURRENT FILING DATE: 2002-06-28
Prior Application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 612
SEQ ID NO 447
LENGTH: 1047
TYPE: DNA
ORGANISM: Homo Saplen
US-10-184-644-447
```

```
Query Match
Best Local Similarity 86.0%; Score 37; DB 9; Length 1047;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
OY 1 CCGKTC 6
DB 631 CCGTTC 636
```

```
RESULT 14
US-10-184-634-447
Sequence 447, Application US/10184634
Publication NO. US2003006864A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Chen, Jian
APPLICANT: Desnoyers, Luc
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Pan, James
APPLICANT: Smith, Victoria
APPLICANT: Watanabe, Collin K.
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P3430R1C217
CURRENT APPLICATION NUMBER: US/10/184,634
CURRENT FILING DATE: 2002-06-28
Prior Application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 612
SEQ ID NO 447
LENGTH: 1047
TYPE: DNA
ORGANISM: Homo Saplen
US-10-184-634-447
```

```
Query Match
Best Local Similarity 86.0%; Score 37; DB 9; Length 1047;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
OY 1 CCGKTC 6
DB 631 CCGTTC 636
```

```
RESULT 15
US-10-184-644-387
Sequence 387, Application US/10184644
Publication NO. US20030044930A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Chen, Jian
APPLICANT: Desnoyers, Luc
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Pan, James
APPLICANT: Smith, Victoria
APPLICANT: Watanabe, Collin K.
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P3430R1C227
CURRENT APPLICATION NUMBER: US/10/184,644
CURRENT FILING DATE: 2002-06-28
Prior Application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 612
SEQ ID NO 387
LENGTH: 1094
TYPE: DNA
ORGANISM: Homo Saplen
US-10-184-644-387
```

```
Query Match
Best Local Similarity 86.0%; Score 37; DB 9; Length 1094;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
OY 1 CCGKTC 6
DB 343 CCGTTC 348
```

```
Search completed: May 6, 2003, 10:36:39
Job time : 18 secs
```

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GenCore version 5.1.4_p5_4578
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: May 6, 2003, 10:27:25 ; Search time 44 Seconds
(without alignments)
13.109 Million cell updates/sec

Title: US-09-555-115a-66

Perfect score: 43

Sequence: 1 CCGKTC 6

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 segs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 08
Maximum Match 100%

Listing first 45 summaries

Database :

1: PIR1:*
2: PIR2:*
3: PIR3:*
4: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	40	93.0	214	2 T19930	hypothetical protein
2	37	86.0	151	2 E48552	US2 protein - infe
3	37	86.0	217	2 A88115	protein F53C3.5 f1
4	37	86.0	324	2 T24819	hypothetical prote
5	37	86.0	370	2 T37282	probable cathepsin
6	37	86.0	597	2 A32440	RNA-directed RNA P
7	37	86.0	1174	2 A39927	genome polyprotein
8	37	86.0	4488	1 RRIHM2	phenylalanine-tRNA
9	36	83.7	339	2 F8614	phenylalanine-tRNA
10	36	83.7	339	2 B72011	phenylalanine-tRNA
11	36	83.7	878	2 E85817	alanyl-tRNA synthet
12	35	81.4	37	2 S30985	gene 40 protein
13	35	81.4	276	2 T49220	casein kinase II (
14	35	81.4	283	2 T01595	casein kinase II (
15	35	81.4	333	2 AB3447	salicylaldehyde de
16	34	79.1	81	2 A45320	transglutaminase s
17	34	79.1	96	2 JE0252	trypsin-6 - bovine
18	34	79.1	146	2 S53010	RCC2 protein - ric
19	34	79.1	146	2 S53011	RCC2 protein - ric
20	34	79.1	151	2 S60314	hair keratin cyste
21	34	79.1	159	2 T33696	hypothetical prote
22	34	79.1	186	2 A45910	ultra-high sulfur
23	34	79.1	186	2 T22278	hypothetical prote
24	34	79.1	190	2 T22279	hypothetical prote
25	34	79.1	192	1 TVGAAC	transforming prote
26	34	79.1	192	2 A5492	GTP-binding protei
27	34	79.1	192	2 S54294	GTP-binding protei
28	34	79.1	192	2 G38625	GTP-binding protei
29	34	79.1	193	1 TVH012	GTP-binding protei

30	34	79.1	193	1 TVB012	GTP-binding protei
31	34	79.1	193	1 TVH0RC	GTP-binding protei
32	34	79.1	193	1 H36364	GTP-binding protei
33	34	79.1	196	1 TVH0RH	GTP-binding protei
34	34	79.1	196	1 TVH0RH	GTP-binding protei
35	34	79.1	196	1 TVH0RH	GTP-binding protei
36	34	79.1	196	1 TVH0RH	GTP-binding protei
37	34	79.1	202	2 JC5075	GTP-binding protei
38	34	79.1	205	2 JC4044	GTP-binding protei
39	34	79.1	205	2 T37769	rhod-1-like protein
40	34	79.1	265	2 T33695	transforming prote
41	34	79.1	340	2 T20148	hypothetical prote
42	34	79.1	346	2 D47211	probable cysteine
43	34	79.1	347	2 T01044	GTP-binding protei
44	34	79.1	400	2 B48613	hypothetical prote
45	34	79.1	591	2 A99444	surface protein SU
			611	2 A48582	acylaminoacyl-pept
					vacuolar ATPase A

ALIGNMENTS

RESULT 1

T19930

hypothetical protein C44C10.9 - Caenorhabditis elegans

C/Species: Caenorhabditis elegans

C/Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 18-Feb-2000

C/Accession: T19930

R/Cottage, A.

submitted to the EMBL Data Library, February 1996

A/Reference number: Z19197

A/Accession: T19930

A/Status: preliminary; translated from GB/EMBL/DBAJ

A/Molecule type: DNA

A/Residues: 1-214 <NTL>

A/Cross-references: EMBL:Z69787; PIDN:CAA93643.1; GSPDB:GN00028; CESP:C44C10.9

A/Experimental source: clone C44C10

C/Genetics:

A/Map position: X

A/Introns: 41/2; 64/2; 99/1; 152/2; 189/2

Query Match

Best Local Similarity 93.0%; Score 40; DB 2; Length 214; Pred. No. 22; Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

DB 48 CCGKTC 53

1 CCGKTC 6

111111

48 CCGKTC 53

1 CCGKTC 6

111111

48 CCGKTC 53

1 CCGKTC 6

111111

48 CCGKTC 53

1 CCGKTC 6

111111

48 CCGKTC 53

1 CCGKTC 6

111111

48 CCGKTC 53

1 CCGKTC 6

111111

48 CCGKTC 53

1 CCGKTC 6

111111

48 CCGKTC 53

1 CCGKTC 6

111111

48 CCGKTC 53

A/Note: sequence extracted from NCBI backbone (NCBI:121622, NCBI:121628)

Query Match 86.0%; Score 37; DB 2; Length 151;

Best Local Similarity 83.3%; Pred. No. 50;

Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

DB 115 CCGKTC 120

1 CCGKTC 6

111111

115 CCGKTC 120

RESULT 3
A88115
protein F53C3.5 [Imported] - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C>Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 10-May-2001
C:Accession: A88115
R:Anonymous, The C. elegans Sequencing Consortium.
S:Science 282, 2012-2018, 1998
A:Title: Genome sequence of the nematode C. elegans: a platform for investigating biology
A:Reference number: A75000; MUID:99069613; PMID:9851916
A>Note: see websites genome.wustl.edu/gsc/C_elegans/ and www.sanger.ac.uk/Projects/C_elegans/
A:Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and
A:Accession: A88115
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-217 <STO>
A:Cross-references: GB:chr_II; PIDN:AC67456.1; PID:93786483; GSPDB:GN00020; CESP:F53C3.5
C:Genetics:
A:Gene: F53C3.5
A:Map position: 2

Query Match 86.0%; Score 37; DB 2; Length 217;
Best Local Similarity 83.3%; Pred. No. 64;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 CCGKTC 6
DB 132 CCGMTC 137

RESULT 4
T24819
hypothetical protein T10H4.12 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 21-Jan-2000
C:Accession: T24819
R:Baisham, V.
A:Submitted to the EMBL Data Library, October 1996
A:Reference number: Z19938
A:Accession: T24819
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-324 <WIL>
A:Cross-references: EMBL:Z81119; PIDN:CA803341.1; GSPDB:GN00023; CESP:T10H4.12
A:Experimental source: clone T10H4
C:Genetics:
A:Gene: CESP:T10H4.12
A:Map position: 5
A:Introns: 184/1; 294/3
C:Superfamily: papain

Query Match 86.0%; Score 37; DB 2; Length 324;
Best Local Similarity 83.3%; Pred. No. 83;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 CCGKTC 6
DB 91 CCGTTC 96

RESULT 5
T37282
probable cathepsin B (EC 3.4.22.1) cpr-3 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C>Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 21-Jul-2000
C:Accession: T37282; T37283
R:Larminie, C.G.; Johnstone, I.L.
S:DNA Cell Biol. 15, 75-82, 1996
A:Title: Isolation and characterization of four developmentally regulated cathepsin B-1
A:Reference number: Z21662; MUID:96152242; PMID:8561899
A:Accession: T37282

A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-370 <LAR>
A:Cross-references: EMBL:L39925; PIDN:AAA98782.1
A:Experimental source: strain Bristol N2
A:Accession: T37283
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-370 <LAZ>
A:Cross-references: EMBL:L39890; NID:9675493; PIDN:AAA98788.1; PID:9675494
A:Experimental source: strain Bristol N2
C:Genetics:
A:Gene: cpr-3
A:Introns: 7/3; 230/1; 340/3
C:Superfamily: papain
C:Keywords: cysteine proteinase; hydrolase
F:120,284,304/active site: Cys, His, Asn #status predicted

Query Match 86.0%; Score 37; DB 2; Length 370;
Best Local Similarity 83.3%; Pred. No. 91;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 CCGKTC 6
DB 153 CCGTTC 158

RESULT 6
A32440
RNA-directed RNA polymerase (EC 2.7.7.48) - murine hepatitis virus (strain A59) (frag
C:Species: murine hepatitis virus, MHV
C>Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 18-Jun-1999
C:Accession: A32440
R:Pachuk, C.J.; Bredenbeek, P.J.; Zoltick, P.W.; Span, W.J.M.; Weiss, S.R.
S:Virology 171, 141-148, 1989
A:Title: Molecular cloning of the gene encoding the putative polymerase of mouse hepa
A:Reference number: A32440; MUID:89299451; PMID:2545027
A:Accession: A32440
A:Molecule type: genomic RNA
A:Residues: 1-597 <PAC>
A:Cross-references: GB:M27198; NID:9928852; PIDN:AAA74011.1; PID:9928854
C:Superfamily: coronavirus RNA-directed RNA polymerase
C:Keywords: nucleotidyltransferase

Query Match 86.0%; Score 37; DB 2; Length 597;
Best Local Similarity 83.3%; Pred. No. 1.2e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 CCGKTC 6
DB 390 CCGTTC 395

RESULT 7
A39927
RNA-directed RNA polymerase (EC 2.7.7.48) - murine hepatitis virus (strain MHV-A59 de
C:Species: murine hepatitis virus, MHV
C>Date: 29-Jan-1993 #sequence_revision 29-Jan-1993 #text_change 25-Oct-1996
C:Accession: A39927
R:van der Most, R.G.; Bredenbeek, P.J.; Spaan, W.J.M.
S:J. Virol. 65, 3219-3226, 1991
A:Title: A domain at the 3' end of the polymerase gene is essential for encapsidation
A:Reference number: A39927; MUID:91237841; PMID:2033672
A:Accession: A39927
A:Molecule type: genomic RNA
A:Residues: 1-1174 <VAN>
A:Cross-references: GB:X57302
A:Note: readthrough of the terminator UAA occurs between the codons GAU for residue 6
C:Superfamily: coronavirus RNA-directed RNA polymerase
C:Keywords: nucleotidyltransferase; RNA binding; RNA biosynthesis

Query Match 86.0%; Score 37; DB 2; Length 1174;
Best Local Similarity 83.3%; Pred. No. 1.9e+02;

Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 CCGKTC 6
11111
Db 22 CCGDTC 27

RESULT 8

genome polypeptide 1a - murine hepatitis virus (strain JHM)
N:Alternate names: 1a protein
N:Contents: RNA-directed RNA polymerase (EC 2.7.7.48)
C:Species: murine hepatitis virus, MHV
C:Date: 30-Sep-1990 #sequence_revision 31-Dec-1992 #text_change 23-Mar-2001
C:Accession: A36815; A34072; A43572
R:Lee, H.J.; Shieh, C.K.; Gorbelenya, A.E.; Koonin, E.V.; La Monica, N.; Tuler, J.; Bagd
submitted to Genbank, February 1991
A:Description: The complete sequence (22 kilobases) of murine coronavirus gene 1 encoding
A:Reference number: A36815
A:Accession: A36815
A:Molecule type: genomic RNA
A:Residues: 1-4488 <LEE>
A:Cross-references: GB:M55148; NID:g3331851; PIDN:AAA46457.1; PID:g3331852
R:Lee, H.J.; Shieh, C.K.; Gorbelenya, A.E.; Koonin, E.V.; La Monica, N.; Tuler, J.; Bagd
Virology 180, 567-582, 1991
A:Title: The complete sequence (22 kilobases) of murine coronavirus gene 1 encoding the
A:Reference number: A38547; MUID:91111976; PMID:1846489
A:Contents: annotation
A:Note: neither nucleotide nor complete amino acid sequence is given
R:See, L.H.; Shieh, C.K.; Baker, S.C.; Chang, M.F.; Lai, M.M.C.
J. Virol. 61, 3968-3976, 1987
A:Title: Sequence and translation of the murine coronavirus 5'-end genomic RNA reveals
A:Reference number: A34072; MUID:8062951; PMID:2824826
A:Accession: A34072
A:Molecule type: genomic RNA
A:Residues: 1-595 <SOE>
A:Cross-references: GB:M18040; NID:g3331873; PIDN:AAA46466.1; PID:g555243
R:Baker, S.C.; La Monica, N.; Shieh, C.K.; Lai, M.M.C.
Adv. Exp. Med. Biol. 276, 283-289, 1990
A:Title: Murine coronavirus gene 1 polypeptide contains an autoproteolytic activity.
A:Reference number: A43572; MUID:91333364; PMID:1966414
A:Accession: A43572
A:Molecule type: genomic RNA
A:Residues: 1038-1343 <BAK>
A:Cross-references: GB:S51684; NID:g234107; PIDN:AA19566.1; PID:g234108
C:Genetics:
A:Gene: 1a
C:Superfamily: coronavirus RNA-directed RNA polymerase
C:Keywords: nucleotidyltransferase; RNA binding; RNA biosynthesis

Query Match

Best Local Similarity 86.0%; Score 37; DB 1; Length 4488;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCGKTC 6
11111
Db 390 CCGDTC 395

RESULT 9

phenylalanyl tRNA synthetase, alpha (imported) - Chlamydia pneumoniae (strain J138)
C:Species: Chlamydia pneumoniae, Chlamydia pneumoniae
C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 23-Mar-2001
C:Accession: F86514
R:Shirai, M.; Hirakawa, H.; Kimoto, M.; Tabuchi, M.; Kishi, F.; Ouchi, K.; Shiba, T.; Ise
Nucleic Acids Res. 28, 2311-2314, 2000
A:Title: Comparison of whole genome sequences of Chlamydia pneumoniae J138.
A:Reference number: A86491; MUID:20330349; PMID:10871362
A:Accession: F86514
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-339 <STO>

A:Cross-references: GB:BA000008; NID:g8979366; PIDN:BA499200.1; GSPDB:GN00142
A:Experimental source: strain J138
C:Genetics:
A:Gene: pheS
C:Superfamily: phenylalanyl-tRNA ligase alpha chain

Query Match 83.7%; Score 36; DB 2; Length 339;
Best Local Similarity 83.3%; Pred. No. 1.2e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCGKTC 6
11111
Db 265 CCGKGC 270

RESULT 10

phenylalanyl-tRNA ligase (EC 6.1.1.20) alpha chain [similarity] - Chlamydia pneumoniae
C:Species: Chlamydia pneumoniae, Chlamydia pneumoniae
C:Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 03-Jun-2002
C:Accession: B72011; F81529
R:Kilman, S.; Mitchell, W.; Marathe, R.; Lammel, C.; Fan, J.; Olinger, L.; Grimwood,
Nature Genet. 21, 385-389, 1999
A:Title: Comparative genomes of Chlamydia pneumoniae and C. trachomatis.
A:Reference number: A72000; MUID:99206606; PMID:10192388
A:Accession: B72011
A:Molecule type: DNA
A:Residues: 1-339 <ARN>
A:Cross-references: GB:AE001679; GB:AE001363; NID:g4377311; PIDN:AMD19130.1; PID:g437
A:Experimental source: strain CWL029
R:Read, T.D.; Brumham, R.C.; Shen, C.; Gill, S.R.; Heidelberg, J.F.; White, O.; Hicke
C.; Dodson, R.; Gwinn, M.; Nelson, W.; Deboy, R.; Kolonay, J.; McClarty, G.; Salzbe
Nucleic Acids Res. 28, 1397-1406, 2000
A:Title: Genome sequences of Chlamydia trachomatis M69 and Chlamydia pneumoniae AR39
A:Reference number: A81500; MUID:20150255; PMID:10684355
A:Accession: F81529
A:Molecule type: DNA
A:Residues: 1-339 <REA>
A:Cross-references: GB:AE002245; GB:AE002161; NID:g7189769; PIDN:AAF38651.1; PID:g718
A:Experimental source: strain AR39, HL cells
C:Genetics:
A:Gene: pheS; CP0862
C:Superfamily: phenylalanyl-tRNA synthetase, alpha chain
C:Keywords: aminoacyl-tRNA synthetase; ligase; protein biosynthesis

Query Match 83.7%; Score 36; DB 2; Length 339;
Best Local Similarity 83.3%; Pred. No. 1.2e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCGKTC 6
11111
Db 265 CCGKGC 270

RESULT 11

alanyl-tRNA synthetase [imported] - Escherichia coli (strain O157:H7, substrain EDL93
C:Species: Escherichia coli
C:Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 14-Sep-2001
C:Accession: E85917
R:Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; May
Nallur, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apoda
Nature 409, 529-533, 2001
A:Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A:Reference number: A85480; MUID:21074935; PMID:11206551
A:Accession: E85917
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-878 <STO>
A:Cross-references: GB:AE005174; NID:g12517136; PIDN:AA657801.1; GSPDB:GN00145; UWGP:
A:Experimental source: strain O157:H7, substrain EDL933
C:Genetics:
A:Gene: alaS

C:Superfamily: alanine-tRNA ligase

Query Match 83.7%; Score 36; DB 2; Length 878;
Best Local Similarity 83.3%; Pred. No. 2.3e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCGKTC 6
|||||
DB 857 CCGKTC 862

RESULT 12

S30985
gene 40 protein - Mycobacterium phage L5
C:Species: Mycobacterium phage L5
C>Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 08-Oct-1999
C:Accession: S30985
R:Donnelly-Wu, M.K.; Jacobs Jr, W.R.; Hatfull, G.F.
Mol. Microbiol. 7, 407-417, 1993
A:Title: Superinfection immunity of mycobacteriophage L5: applications for genetic trans
A:Reference number: S30949; MUID:93211283; PMID:8459767
A:Accession: S30985
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-37 <DON>
A:Cross-References: EMBL:Z18946; NID:g15859; PIDN:CAA79416.1; PID:g15896
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, December 1992
C:Genetics:
A:Gene: 40

Query Match 81.4%; Score 35; DB 2; Length 37;
Best Local Similarity 83.3%; Pred. No. 40;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCGKTC 6
|||||
DB 21 CCGKTC 26

RESULT 13

T49220
casein kinase II (EC 2.7.1.-) beta chain CKB3 [validated] - Arabidopsis thaliana
M:Alternate names: protein F27H5.40
C:Species: Arabidopsis thaliana (mouse-ear cress)
C>Date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 03-Nov-2000
C:Accession: T49220; T52032
R:Rieger, M.; Mueller-Auer, S.; Zipp, M.; Schaefer, M.; Mewes, H.W.; Rudd, S.; Lemcke, K.
submitted to the Protein Sequence Database, April 2000
A:Reference number: Z25018
A:Accession: T49220
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-276 <RIE>
A:Cross-References: EMBL:AL163852; GSPDB:GN00061; ATSP:F27H5.40
A:Experimental source: cultivar Columbia; BAC clone F27H5
R:Sugano, S.; Andronis, C.; Green, R.M.; Wang, Z.Y.; Todin, E.M.
Proc. Natl. Acad. Sci. U.S.A. 95, 11020-5, 1998
A:Title: Protein kinase CK2 interacts with and phosphorylates the Arabidopsis circadian
A:Reference number: Z24495; MUID:9724832; PMID:9724822
A:Accession: T52032
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-276 <STUG>
A:Cross-References: EMBL:AF068318; PIDN:AAC33896.1
C:Genetics:
A:Gene: ATSP:F27H5.40
A:Map position: 3
A:Introns: 69/1; 142/1; 178/3; 234/1
A:Note: CKB3
C:Function:
A:Description: interacts specifically with circadian clock-associated 1 (CCL1) [validated]
A:Note: CKB3 is the only reported example of a third beta-subunit of CK2 found in any or
C:Superfamily: human casein kinase II beta chain

C:Keywords: phosphotransferase

Query Match 81.4%; Score 35; DB 2; Length 276;
Best Local Similarity 66.7%; Pred. No. 1.5e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCGKTC 6
|||||
DB 195 CCGKTC 200

RESULT 14

T01595
casein kinase II (EC 2.7.1.-) beta chain At2g44680 - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C>Date: 19-Feb-1999 #sequence_revision 19-Feb-1999 #text_change 16-Feb-2001
C:Accession: T01595; E84881
R:Rounsley, S.D.; Kaul, S.; Lin, X.; Ketchum, K.A.; Crosby, M.L.; Brandon, R.C.; Syke
submitted to the EMBL Data Library, July 1998
A:Description: Arabidopsis thaliana chromosome II BAC F16R22 genomic sequence.
A:Reference number: Z14284
A:Accession: T01595
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-283 <ROU>
A:Cross-References: EMBL:AC003672; NID:g3341671; PID:g3341688
A:Experimental source: cultivar Columbia
R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanKen, S.E.; Umayam, L.; Tallon,
euss, D.; Nieman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter
Nature 402, 761-768, 1999
A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A:Reference number: A84420; MUID:20083487; PMID:10617197
A:Accession: E84881

Query Match 81.4%; Score 35; DB 2; Length 283;
Best Local Similarity 66.7%; Pred. No. 1.5e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCGKTC 6
|||||
DB 201 CCGKTC 206

RESULT 15

AB3447
salicylaldehyde dehydrogenase (EC 1.-.-) [imported] - Brucella melitensis (strain 1
C:Species: Brucella melitensis
C>Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 01-Feb-2002
C:Accession: AB3447
R:DelVecchio, V.G.; Kapural, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanov,
.; Mazur, M.; Goldsman, E.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Let
Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002
A:Title: The genome sequence of the facultative intracellular pathogen Brucella melit
A:Reference number: AD3252; PMID:11756688
A:Accession: AB3447
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-333 <KUR>
A:Cross-References: GB:AE008917; PIDN:AAL52741.1; PID:g17983572; GSPDB:GN00190
A:Experimental source: strain 16M
C:Genetics:
A:Gene: BME11560

A:Map position: I
C:Keywords: oxidoreductase

Query Match 81.4%; Score 35; DB 2; Length 333;
Best Local Similarity 66.7%; Pred No. 1.7e+02;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Oy 1 CCGKTC 6
111: 1
Db 12 CCGRAC 17

Search completed: May 6, 2003, 10:31:52
Job time : 47 secs

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GenCore version 5.1.4-p5-4578
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OM protein - protein search, using sw model

Run on: May 6, 2003, 10:17:40 ; Search time 11 Seconds
(without alignments)
22.623 Million cell updates/sec

Title: US-09-555-115A-66

Perfect score: 43

Sequence: 1 CCGKTC 6

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	38	88.4	64	1 MTCU_CALSI
2	37	86.0	151	1 D453_HSVNG
3	37	86.0	370	1 CRR3_CABEL
4	37	86.0	597	1 RRP3_CWMA5
5	37	86.0	4488	1 RRP3_CWMA5
6	36	83.7	339	1 SYFA_CHUPN
7	35	81.4	37	1 VG40_BHML5
8	35	81.4	276	1 KC2D_ARATH
9	35	81.4	283	1 KC2E_ARATH
10	35	81.4	627	1 TRGS_MOUSE
11	34	79.1	81	1 INL4_DROME
12	34	79.1	154	1 INL4_DROME
13	34	79.1	192	1 RHO1_DROME
14	34	79.1	192	1 RHO1_DROME
15	34	79.1	192	1 RHO1_DROME
16	34	79.1	192	1 RHO1_DROME
17	34	79.1	193	1 RHO1_DROME
18	34	79.1	193	1 RHO1_DROME
19	34	79.1	193	1 RHO1_DROME
20	34	79.1	193	1 RHO1_DROME
21	34	79.1	193	1 RHO1_DROME
22	34	79.1	196	1 RHO1_DROME
23	34	79.1	198	1 RHO1_DROME
24	34	79.1	202	1 RHO1_DROME
25	34	79.1	209	1 RHO1_DROME
26	34	79.1	329	1 CYS1_CABEL
27	34	79.1	346	1 CYS1_CABEL
28	34	79.1	611	1 VATA_PLAFA
29	34	79.1	885	1 TRP2_RAT
30	34	79.1	1032	1 ITA4_XENIA
31	34	79.1	1035	1 ITA4_XENIA
32	34	79.1	1038	1 ITA4_XENIA
33	34	79.1	1039	1 ITA4_XENIA

34	34	79.1	1172	1 TRP2_MOUSE	09244 mus musculu
35	34	79.1	3718	1 LMA5_MOUSE	061001 mus musculu
36	34	76.7	37	1 TXOD_HADVE	P81597 hadronyche
37	33	76.7	60	1 MTA_CHAAC	093593 chaenocarpa
38	33	76.7	76	1 VF07_VACCV	P24359 vaccinia vl
39	33	76.7	79	1 VF07_VACCV	P33867 vacinola vit
40	33	76.7	80	1 VF07_VACCV	P29886 vaccinia vl
41	33	76.7	92	1 VF07_VACCV	P21016 vaccinia vl
42	33	76.7	102	1 ELAC_TRIVU	029143 trichosurus
43	33	76.7	282	1 KC2C_ARATH	P40229 arabidopsis
44	33	76.7	287	1 KC2E_ARATH	P40228 arabidopsis
45	33	76.7	324	1 Y734_CHUPN	Q927H1 chlamydia p

ALIGNMENTS

RESULT 1	MTCU_CALSI	STANDARD;	PRT;	64 AA.
ID	MTCU_CALSI			
AC	090620;			
DT	16-OCT-2001 (Rel. 40, Created)			
DT	16-OCT-2001 (Rel. 40, Last sequence update)			
DT	15-JUN-2002 (Rel. 41, Last annotation update)			
DE	Copper-specific metallothionein 2 (CuMT-II).			
OS	Callinectes sapidus (Blue crab).			
OC	Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Crustacea;			
OC	Malacostraca; Eumalacostraca; Eucarida; Decapoda; Pleocyemata;			
OC	Brachyura; Eubrachyura; Portunoidae; Portunidae; Callinectes.			
OX	NCBI_TaxID=6763;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=20356402; PubMed=10817938;			
RA	Syring R.A., Hoexum-Brouwer T.H., Brouwer M.;			
RT	Cloning and sequencing of cDNAs encoding for a novel copper-specific			
RT	metallothionein and two cadmium-inducible metallothioneins from the			
RT	blue crab Callinectes sapidus.			
RL	Comp. Biochem. Physiol. 125C:325-332(2000).			
CC	-1- FUNCTION: THE METALLOTHIONEINS ARE INVOLVED IN THE CELLULAR			
CC	SEQUESTRATION OF TOXIC METAL IONS AND REGULATION OF ESSENTIAL			
CC	TRACE ELEMENTS. THIS ISOFORM BINDS EXCLUSIVELY COPPER.			
CC	-1- DOMAIN: 14 CYSTEINE RESIDUES ARE ARRANGED IN C-X-C GROUPS. THESE			
CC	ARE THOUGHT TO BE THE METAL-BINDING SITES IN OTHER			
CC	METALLOTHIONEINS.			
CC	-1- SIMILARITY: BELONGS TO THE METALLOTHIONEIN SUPERFAMILY; FAMILY 2.			
CC	THIS SWISS-PROT entry is copyright. It is produced through a collaboration			
CC	between the Swiss Institute of Bioinformatics and the EMBL Outstation -			
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CC	use by non-profit institutions as long as its content is in no way			
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CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/			
CC	or send an email to license@sib-sib.ch).			
CC	EMBL: AF200420; AAF08966.1; -			
DR	InterPro: IPR001008; Mtlthion_musc.			
DR	InterPro: IPR001230; Prenyl_site.			
DR	PRINTS: PR00875; MTMOUSC.			
KW	Metal-binding; Metal-chelate cluster; Copper.			
SO	SEQUENCE 64 AA: 6277 MW; B0B8767AD6CEB78A CRR64;			
QY	Query Match	88.4%;	Score 38;	DB 1;
QY	Best local Similarity	83.3%;	Pred. No. 7;	
QY	Matches 5;	Conservative 0;	Mismatches 1;	Indels 0;
QY	1 CCGKTC 6			
QY	11111			
QY	17 CCGSTC 22			
DB	17 CCGSTC 22			
RESULT 2	U453_HSVNG	STANDARD;	PRT;	151 AA.
ID	U453_HSVNG			

AC 005106: 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 01-FEB-1995 (Rel. 31, Last annotation update)
DE Hypothetical 16.6 kDa protein.
GN US453.
OS Marek's disease herpesvirus (strain GA) (MDHV).
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC Alphaherpesvirinae; Marek's disease-like viruses.
OX NCBI_TaxID=10388;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93118245; PubMed=1282282;
RA Sarguchel M., Urakawa T., Hirayama Y., Miki N., Yamamoto M.,
Hirai K.;
RT "Sequence determination and genetic content of an 8.9-kb restriction
fragment in the short unique region and the internal inverted repeat
of Marek's disease virus type 1 DNA."
RT Virus Genes 6:365-378(1992).
CC -----
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CC -----
DR EMBL: M80595; AAB59894.1; -;
DR InterPro: IPR003485; Us2_Unk.
DR Pfam: PF02476; US2; 1.
KM Hypothetical protein.
SQ SEQUENCE 151 AA; 16635 MW; 5039D9E32D0D344C CRC64;
OY 1 CCGKTC 6
DB 115 CCGKCC 120
Query Match Best Local Similarity 86.0%; Score 37; DB 1; Length 151;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
RESULT 3
CPR3_CAEEL STANDARD; PRT; 370 AA.
AC P43507; Q9TW93;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Cathepsin B-like cysteine proteinase 3 precursor (EC 3.4.22.-)
DE (Cysteine protease related 3).
GN CPR-3 OR T10H4.12.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-Bristol NZ;
RA Lamine C.G.C., Johnstone I.L.;
RL Submitted (MAR-1995) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-Bristol NZ;
RA Baahm V.M.;
RL Submitted (OCT-1996) to the EMBL/GenBank/DBJ databases.
RN [3]
REVIEWS:
RA Dublin R.;
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY C1.
CC -----

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CC -----
DR EMBL: L39890; AAA98788.1; -;
DR EMBL: L39925; AAA98782.1; -;
DR EMBL: 281119; CAB61032.2; -;
DR EMBL: 282057; CAB61032.2; JOINED.
DR EMBL: 282057; CAB61024.2; -;
DR EMBL: 281119; CAB61024.2; JOINED.
DR HSSP: P07688; 10DQ.
DR MEROPS: C01.0PA; -;
DR WormRep: T10H4.12; CE27590.
DR InterPro: IPR000668; Peptidase_C1.
DR InterPro: IPR000169; SHProt_acsite.
DR Pfam: PF00112; Peptidase_C1; 1.
DR PRINTS: PR00705; PAPA1N.
DR ProDom: PD000158; Peptidase_C1; 1.
DR PROSITE: PS00139; THIOL_PROTEASE_CYS; 1.
DR PROSITE: PS00639; THIOL_PROTEASE_HIS; 1.
DR PROSITE: PS00640; THIOL_PROTEASE_ASN; 1.
KM Hydrolyase; Thiol protease; zymogen; signal.
FT SIGNAL 1
FT PROPEP 17 91
FT CHAIN 92 370
FT ACT_SITE 120 120
FT ACT_SITE 284 284
FT ACT_SITE 304 304
FT ACT_SITE 105 134
FT DISULFID 117 162
FT DISULFID 153 210
FT DISULFID 154 158
FT DISULFID 190 214
FT DISULFID 198 202
FT CARBOHYD 138 138
SQ SEQUENCE 370 AA; 40770 MW; E6E50FE7C16F0867 CRC64;
OY 1 CCGKTC 6
DB 153 CCGTTC 158
Query Match Best Local Similarity 86.0%; Score 37; DB 1; Length 370;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
RESULT 4
RRPA_CVMA5 STANDARD; PRT; 597 AA.
ID RRPA_CVMA5
AC P19750;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE RNA-directed RNA polymerase (ORF1A) (EC 2.7.7.48) (Fragment).
OS Murine coronavirus MHV (strain A59).
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;
OC Coronaviridae; Coronavirus.
OX NCBI_TaxID=11142;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=89299451; PubMed=2545027;
RA Pachuk C.J., Bredenbeek P.J., Zoltick P.W., Spaan W.J.M., Weiss S.R.;
RT "Molecular cloning of the gene encoding the putative polymerase of
mouse hepatitis coronavirus, strain A59."
RL Virology 171:141-148(1989).
CC -1- FUNCTION: THE RNA DEPENDENT RNA POLYMERASE OF CORONAVIRUSES IS
CC A MULTIFUNCTIONAL PROTEIN. IT CONTAINS THE ACTIVITIES NECESSARY
CC FOR THE TRANSCRIPTION OF NEGATIVE STRANDED RNA, LEADER RNA,
CC SUBGENOMIC MRNAs AND PROGENY VIRION RNA.
CC -----

CC -1- CATALYTIC ACTIVITY: N nucleoside triphosphate - N diphosphate +
CC (RNA)(N).
CC -----
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CC -----
DR EMBL: M27198; AAA74011.1; -
DR PIR: A32440; A32440.
KW Transferase: RNA-directed RNA polymerase.
FT NON_TER 597 597
SQ SEQUENCE 597 AA; 66193 MW; 165D4FACAA33BC49E CRC64;

Query Match 86.0%; Score 37; DB 1; Length 597;
Best Local Similarity 83.3%; Pred. No. 48;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCGKTC 6
ID III II
Db 390 CCGDTC 395

RESULT 5
RRA_CVMJH STANDARD; PRT; 4488 AA.
AC P19751; 066194; -
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE RNA-directed RNA polymerase (ORF1A) (EC 2.7.7.48).
OS Murine coronavirus MHV (strain JHM).
OC Viruses: ssRNA positive-strand viruses, no DNA stage; Nidovirales;
OC Coronaviridae; Coronavirus.
OX NCBI_TaxID=11144;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-9111976; PubMed-1846489;
RA Lee H.-J., Shieh C.-K., Gorbalenya A.E., Koonin E.V., Ia Monica N.,
RA Tuler J., Bagdzhadzyan A., Lai M.-M.C.;
RT The complete sequence (22 kilobases) of murine coronavirus gene 1
RT encoding the putative proteases and RNA polymerase.";
RL Virology 180:567-582(1991).
RN [2]
RP SEQUENCE OF 1-595 FROM N.A.
RX MEDLINE-88062951; PubMed-2824826;
RA Soe L.H., Shieh C.K., Baker S.C., Chang M.F., Lai M.-M.C.;
RT "Sequence and translation of the murine coronavirus 5'-end genomic
RT RNA reveals the N-terminal structure of the putative RNA
RT polymerase.";
RL J. Virol. 61:3968-3976(1987).
RN [3]
RP FUNCTION: THE RNA DEPENDENT RNA POLYMERASE OF CORONAVIRUSES IS
RP A MULTIFUNCTIONAL PROTEIN: IT CONTAINS THE ACTIVITIES NECESSARY
RP FOR THE TRANSCRIPTION OF NEGATIVE STRANDED RNA, LEADER RNA,
RP SUBGENOMIC MRNAS AND PROGENY VIRION RNA.
CC -1- CATALYTIC ACTIVITY: N nucleoside triphosphate - N diphosphate +
CC (RNA)(N).
CC -----
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CC -----
DR EMBL: M55148; AAA6457.1; -
DR EMBL: M18040; AAA6466.1; -
DR PIR: A36815; RRIHM2.
DR MEROPS: C16.001; -

DR MEROPS: C29.001; -
DR DR MEROPS: C30.001; -
DR InterPro: IPR002589; Alpp.
DR InterPro: IPR002705; Peptidase_C16.
DR Pfam: PF01661; Alpp; 1.
DR Pfam: PF01831; Peptidase_C16; 1.
DR SMART: SM00506; Alpp; 1.
KW Transferase: RNA-directed RNA polymerase.
SQ SEQUENCE 4488 AA; 499890 MW; D9EE61A9E2141799 CRC64;

Query Match 86.0%; Score 37; DB 1; Length 4488;
Best Local Similarity 83.3%; Pred. No. 2e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCGKTC 6
ID III II
Db 390 CCGDTC 395

RESULT 6
SYFA_CHLPN STANDARD; PRT; 339 AA.
AC 0926R6;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Phenylalanine-tRNA synthetase alpha chain (EC 6.1.1.20) (Phenylalanine-
DE -tRNA ligase alpha chain) (PheRS).
GN PHE-OR CPN0993 OR CP0862.
OS Chlamydia pneumoniae (Chlamydia pneumoniae).
OC Bacteria; Chlamydiales; Chlamydiaceae; Chlamydia.
OX NCBI_TaxID=83558;
RN [1]
RP SEQUENCE FROM N.A.
RX SPRAIN-CM1029.
RC MEDLINE-99206606; PubMed-10192388;
RA Kaiman S., Mitchell W., Marathe R., Lammell C., Fan J., Hyman R.W.,
RA Olinger L., Grimwood J., Davis R.W., Stephens R.S.;
RT "Comparative genomes of Chlamydia pneumoniae and C. trachomatis.";
RL Nat. Genet. 21:385-389(1999).
RN [2]
RP SEQUENCE FROM N.A.
RX STRAIN-AR39.
RC MEDLINE-20150255; PubMed-10684935;
RA Read T.D., Brunham R.C., Shen C., Gill S.R., Heidelberg J.F.,
RA White O., Hickey E.K., Peterson J., Ufferback T., Berry K., Bass S.,
RA Linher K., Weidman J., Khouri H., Craven B., Bowman C., Dodson R.,
RA Gwin M., Nelson W., Deboy R., Kolony J., McClarty G., Salzberg S.L.,
RA Eisen J., Fraser C.M.;
RT "Genome sequences of Chlamydia trachomatis Mopn and Chlamydia
RT pneumoniae AR39.";
RL Nucleic Acids Res. 28:1397-1406(2000).
RN [3]
RP SEQUENCE FROM N.A.
RX STRAIN-Q138;
RC MEDLINE-2030349; PubMed-10871362;
RA Shirai M., Hirakawa H., Kimoto M., Tabuchi M., Kishi F., Ouchi K.,
RA Shiba T., Ishi K., Hattori M., Kubara S., Nakazawa T.;
RT "Comparison of whole genome sequences of Chlamydia pneumoniae J138
RT from Japan and CM1029 from USA.";
RL Nucleic Acids Res. 28:2311-2314(2000).
RN [4]
RP -1- CATALYTIC ACTIVITY: ATP + L-phenylalanine + tRNA(Phe) - AMP +
RP diphosphate + L-phenylalanine-tRNA(Phe).
CC -1- SUBUNIT: Tetramer of two alpha and two beta chains (BY
CC SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC -1- SIMILARITY: BELONGS TO CLASS-II AMINOACYL-TRNA SYNTHETASE FAMILY.
CC PHE-TRNA SYNTHETASE ALPHA CHAIN SUBFAMILY 1.
CC -----
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CC EMBL, AE001679; AAD19130.1; -
 CC EMBL, AE002245; AAF38651.1; -
 DR EMBL, AP002548; BAA99200.1; -
 DR HSSP, F27001; 1B7Y.
 DR TIGR, CP0862; -
 DR InterPro: IPR002106; ALCRNA_ligaseII.
 DR InterPro: IPR004529; Phes.
 DR InterPro: IPR004188; Phe_tRNA_synth_N.
 DR InterPro: IPR002319; tRNA-synth_2d.
 DR Pfam: PF01409; tRNA-synth_2d; 1.
 DR TIGRfams: TIGR00468; Phes; 1.
 DR PROSITE: PS00862; AA.TRNA.LIGASE.II; 1.
 KW Aminoacyl-tRNA synthetase; Protein biosynthesis; Ligase; ATP-binding;
 KW Complete proteome.
 SQ SEQUENCE 339 AA; 38366 MW; D7BA5917EAD9C2A CRC64;

Query Match 83.7%; Score 36; DB 1; Length 339;
 Best Local Similarity 83.3%; Pred. No. 46;
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCGKTC 6
 DB 265 CCGKTC 270

RESULT 7
 VC40_BPML5 STANDARD; PRT; 37 AA.
 ID VG40_BPML5
 OC 005250;
 DT 01-FEB-1994 (Rel. 28, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 01-FEB-1994 (Rel. 28, Last annotation update)
 DE Gene 40 protein (GP40).
 GN 40.
 OS Mycobacteriophage L5.
 OC Viruses: dsDNA viruses, no RNA stage; Caudovirales; Siphoviridae;
 OC L5-like viruses.
 OX NCBI_TaxID=31757;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=93211282; PubMed=8459766;
 RA Hatfull G.F., Sarkis G.J.;
 RT "DNA sequence, structure and gene expression of mycobacteriophage L5:
 RT a phage system for mycobacterial genetics.";
 RL Mol. Microbiol. 7:395-405(1993).

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CC EMBL, 218946; CAA79416.1; -
 DR PIR, S30985; S30985.
 DR SEQUENCE 37 AA; 4444 MW; 0A3696C8418AFCE CRC64;

Query Match 81.4%; Score 35; DB 1; Length 37;
 Best Local Similarity 83.3%; Pred. No. 13;
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCGKTC 6
 DB 21 CCGKTC 26

RESULT 8

KC2D_ARATH STANDARD; PRT; 276 AA.
 ID KC2D_ARATH
 AC 081275;
 DT 15-JUL-1999 (Rel. 38, Created)
 DT 15-JUL-1999 (Rel. 38, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE CKB3 OR AT3G60250 OR F27H5_40.
 GN Arabidopsis thaliana (Mouse-ear cress).
 OS Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.
 OX NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98393763; PubMed=9724822;
 RA Sugeno S., Andronis C., Green R.M., Wang Z.Y., Tobin E.M.;
 RT "Protein Kinase CK2 interacts with and phosphorylates the Arabidopsis
 RT circadian clock-associated 1 protein.";
 RL Proc. Natl. Acad. Sci. U.S.A. 95:11020-11025(1998).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Columbia;
 RX MEDLINE=21016720; PubMed=11130713;
 RA Salanoubat M., Lemcke K., Rieger M., Ansoerge W., Unselid M.,
 RA Faltmann B., Valle G., Bloeker H., Perez-Alonso M., Obermayer B.,
 RA Delensy M., Boutry M., Griwall L.A., Mache R., Pulgomech P.,
 RA De Simone V., Cholsne N., Artiguenave F., Robert C., Brottier P.,
 RA Wincker P., Cattolico L., Weisenbach J., Saurin W., Queller F.,
 RA Schaefer M., Mueller-Auer S., Gabel C., Fuchs M., Benes V.,
 RA Wurdach E., Drzonek H., Erle H., Jordan N., Bangert S.,
 RA Wiedelmann R., Kranz H., Voss H., Holland R., Brandt P., Nyakatura G.,
 RA Vezzi A., D'Angelo M., Pallavicini A., Toppo S., Simonati B.,
 RA Conrad A., Hornischer K., Kauer G., Loehner T.-H., Nordstiek G.,
 RA Reichelt J., Scharfe M., Schoen O., Barges M., Terol J., Clement J.,
 RA Navarro P., Collado C., Perez-Perez A., Ottenweider B., Duchemin D.,
 RA Cooke R., Lande M., Berger-Liauro C., Purnelle B., Masny D.,
 RA de Haan M., Maarse A.C., Alcaraz J.-P., Cottet A., Casacuberta E.,
 RA Monfort A., Argitrou A., Flores M., Liguori R., Vitale D.,
 RA Manhaupt G., Haase D., Schoof H., Rudd S., Zaccaria P., Mewes H.-W.,
 RA Mayer K.F.X., Kaul S., Town C.D., Koo H.L., Tallon L.J., Jenkins J.,
 RA Rooney T., Rizzo M., Walts A., Uterback T., Fujii C.Y., Shea T.P.,
 RA Creasy T.H., Haas B., Maiti R., Wu D., Peterson J., Van Aken S.,
 RA Pal G., Miltischer J., Sellers P., Gall J.E., Feldlyum T.V.,
 RA Preuss D., Lin X., Nierman W.C., Salzberg S.L., White O., Venter J.C.,
 RA Fraser C.M., Kaneo T., Nakamura Y., Sato S., Kato T., Asamizu E.,
 RA Sasamoto S., Kimura T., Idesawa K., Kawashima K., Kishida Y.,
 RA Kiyokawa C., Kohara M., Matsunoto M., Matsuno A., Muraki A.,
 RA Nakayama S., Nakazaki N., Shinpo S., Takeuchi C., Wada T.,
 RA Watanabe A., Yamada M., Yasuda M., Tabata S.;
 RT "Sequence and analysis of chromosome 3 of the plant Arabidopsis
 RT thaliana.";
 RL Nature 406:820-822(2000).
 CC -1- FUNCTION: PLAYS A COMPLEX ROLE IN REGULATING THE BASAL CATALYTIC
 CC ACTIVITY OF THE ALPHA SUBUNIT (BY SIMILARITY).
 CC -1- SUBUNIT: TETRAMER COMPOSED OF AN ALPHA CHAIN, AN ALPHA', AND
 CC TWO BETA-TYPE CHAINS.
 CC -1- SIMILARITY: BELONGS TO THE CASEIN KINASE 2 BETA CHAIN FAMILY.
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CC EMBL, AF068318; AAC33896.1; -
 DR EMBL, AL163852; CAB87862.1; -
 DR TRANSFAC: T02899; -
 DR InterPro: IPR000704; CAS_kinase_II.
 DR Pfam: PF01214; CK_II_beta; 1.

NCBI_TaxID=7227;
 [1]
 SEQUENCE FROM N.A.
 MEDLINE=95137009; PubMed=7835340;
 Harharan I.K., Hu K.-Q., Asha H., Quintanilla A., Ezzell R.M.,
 Settlemann J.,
 "Characterization of rho GTPase family homologues in Drosophila
 melanogaster: overexpressing Rho1 in retinal cells causes a late
 developmental defect.";
 RT EMO J. 14:292-302(1995).
 [2]
 SEQUENCE FROM N.A.
 MEDLINE=20025394; PubMed=10556060;
 Magle C.R., Meyer M.R., Gorsuch M.S., Parkhurst S.M.,
 "Mutations in the Rho1 small GTPase disrupt morphogenesis and
 segmentation during early Drosophila development.";
 RT Development 126:5353-5364(1999).
 [3]
 SEQUENCE FROM N.A.
 STRAIN=Berkeley;
 MEDLINE=20196006; PubMed=10731132;
 Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
 George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 Sutton G.G., Wortman J.R., Fandell M.D., Zhang Q., Chen L.X.,
 Brandon R.C., Rogers Y.-H.C., Blazer R.G., Champe M., Pfeiffer B.D.,
 Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Milos G.L.G.,
 Abiri J.F., Agbayani A., An H.-J., Andrews-Pfankoch C., Baldwin D.,
 Ballwe R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
 Borokva D., Botchan M.R., Bouck J., Brokstein P., Brotler J.,
 Burlas K.C., Busan D.A., Butler H., Cadieu E., Center A., Chandra I.,
 Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 Dodson K., Dou P.L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
 Fosler C., Gabrielian A.E., Gary N.S., Gelbart W.M., Glasser K.,
 Glodok E., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
 Jostall D., Houston K.A., Howland T.J., Wei M.-H., Idegawa C.,
 Jallil M., Kalush F., Kapen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kuip D., Lai Z.,
 Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 Merkulov G., Milshina N.V., Moharry C., Morris J., Moshrefi A.,
 Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Paclib J.M.,
 Palazolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 Spletter E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 Sylvestre R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 Wang Z.-Y., Wasserman D.A., Weinstock G.M., Welschbach J.,
 Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 Ye J., Yeh R.F., Zaveri J.S., Zhan W., Zhang G., Zhao X., Zheng L.,
 Zheng X.H., Zhong F.N., Zhong X., Zhou X., Zhu S., Zhu X., Smith H.O.,
 Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 "The genome sequence of Drosophila melanogaster.";
 RT Science 287:2185-2195(2000).
 [1- SIMILARITY: BELONGS TO THE SMALL GTPASE SUPERFAMILY. RHO FAMILY.

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 EMBL: L38311; AAA67042.1; -
 EMBL: AF177872; AAF01183.1; -
 EMBL: AF177873; AAF01184.1; -
 EMBL: AF177873; AAF01185.1; -

EMBL: AF177874; AAF01186.1; -
 DR EMBL: AEO03808; AAF58066.1; -
 DR HSSP: P06749; 1FTN.
 DR FLYBASE: FBgn0014020; Rho1.
 DR InterPro: IPR003578; GTPase_Rho.
 DR InterPro: IPR001230; Prenyl_site.
 DR InterPro: IPR001806; Ras_crimming.
 DR InterPro: IPR005225; Small_GTP.
 DR Pfam: PF000071; ras; 1.
 DR Pfam: PR00449; RASTRNSFRMNG.
 DR SMART: SM00174; RHO; 1.
 DR TIGRfam: TIGR00231; small_GTP; 1.
 KW GTP-binding; Prenylation; Lipoprotein.
 FT NE_BIND 12 19 GTP (BY SIMILARITY).
 FT NE_BIND 59 63 GTP (BY SIMILARITY).
 FT NE_BIND 117 120 GTP (BY SIMILARITY).
 FT DOMAIN 34 42 EFFECTOR REGION (POTENTIAL).
 FT LIPID 189 189 GERANYL-GERANYL (BY SIMILARITY).
 FT SEQUENCE 192 AA; 21723 MW; B89C7DB84E1743CF CRC64;
 SQ
 Query Match 79.1%; Score 34; DB 1; Length 192;
 Best Local Similarity 100.0%; Pred. No. 61;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 CGKTC 6
 DB 16 CGKTC 20
 ID RHOA_CAEEL STANDARD; PRT; 192 AA.
 AC Q22038;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE RAS-like GTP-binding protein RhoA.
 GN RHO-1 OR RHOA OR Y51H4A.3.
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;
 OC Rhabditidae; Meloiderinae; Caenorhabditis.
 OC NCBI_TaxID=6239;
 RX MEDLINE=95096090; PubMed=7798239;
 RA Chen W., Lim L.;
 RT "The Caenorhabditis elegans small GTP-binding protein RhoA is
 RT enriched in the nerve ring and sensory neurons during larval
 RT development.";
 RT J. Biol. Chem. 269:32394-32404(1994).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-Bristol N2;
 RA Submitted (OCT-1993) to the EMBL/GenBank/DBJ databases.
 RL CYTOSKELETON LOCATION: ASSOCIATED WITH THE MEMBRANE AND THE
 CC CYTOSKELETON THROUGHOUT DEVELOPMENT.
 CC [1- DEVELOPMENTAL STAGE: UNOBTAINED EXPRESSION THROUGHOUT DEVELOPMENT
 CC WITH A PARTICULAR ENRICHMENT AT LARVAL STAGES IN THE PHARYNGEAL
 CC NERVE RING AND AT THE TIP OF THE HEAD CONTAINING CHEMOSENSORY AND
 CC MECHANOSENSORY NEURONS.
 CC [1- SIMILARITY: BELONGS TO THE SMALL GTPASE SUPERFAMILY. RHO FAMILY.

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 EMBL: L36965; AAC37216.1; -

DR EMBL: A1132952; CAB63379.1; -.
 DR HSSP: P06749; IFTN.
 DR Wormpep: Y51H4A.3; CE25369.
 DR InterPro: IPR003578; GTPase_Rho.
 DR InterPro: IPR001230; Prenyl_site.
 DR InterPro: IPR001806; Ras_trnsfrmg.
 DR InterPro: IPR005225; Small_GTP.
 DR Pfam: PF00071; ras; 1.
 DR PRINTS: PR00449; RASTRNSFRMNG.
 DR SMART: SM00174; RHO; 1.
 DR TIGRFAMS: TIGR00231; small_GTP; 1.
 DR GTP-binding; Prenylation; Lipoprotein.
 FT NP_BIND 12 19 GTP (BY SIMILARITY).
 FT NP_BIND 59 63 GTP (BY SIMILARITY).
 FT NP_BIND 117 120 GTP (BY SIMILARITY).
 FT DOMAIN 34 42 GTP (BY SIMILARITY).
 FT LIPID 189 189 EFFECTOR REGION (POTENTIAL).
 FT LIPID 189 189 GERANYL-GERANYL (BY SIMILARITY).
 SQ SEQUENCE 192 AA; 21635 MW; 0B10A744BD0CF81 CRC64;

Query Match 79.1%; Score 34; DB 1; Length 192;
 Best Local Similarity 100.0%; Pred. No. 61;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 CGKTC 6
 |||||
 DB 16 CGKTC 20

RESULT 15
 RHO_APLCA
 ID RHO_APLCA STANDARD; PRT; 192 AA.
 AC P01122; 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 01-OCT-1994 (Rel. 30, Last annotation update)
 DE RAS-like GTP-binding protein RHO.
 GN RHO.
 OS Aplysia californica (California sea hare).
 OC Eukaryota; Metazoa; Mollusca; Gastropoda; Opisthobranchia; Anaspidia;
 OC Aplysidae; Aplysia.
 OX NCBI_TaxID=6500;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=85201682; PubMed=3888408;
 RA Madanle P., Axel R.;
 RT "A novel ras-related gene family.";
 RL Cell 41:31-40(1985).
 CC -1 SIMILARITY: BELONGS TO THE SMALL GTPASE SUPERFAMILY. RHO FAMILY.
 CC -----
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 CC -----
 CC EMBL: M10078; AAA27776.1; -.
 DR PIR: A01373; TVGAC.
 DR HSSP: P06749; IFTN.
 DR InterPro: IPR003578; GTPase_Rho.
 DR InterPro: IPR001230; Prenyl_site.
 DR InterPro: IPR001806; Ras_trnsfrmg.
 DR Pfam: PF00071; ras; 1.
 DR PRINTS: PR00449; RASTRNSFRMNG.
 DR SMART: SM00174; RHO; 1.
 DR TIGRFAMS: TIGR00231; small_GTP; 1.
 DR GTP-binding; Prenylation; Lipoprotein.
 FT NP_BIND 12 19 GTP (BY SIMILARITY).
 FT NP_BIND 59 63 GTP (BY SIMILARITY).
 FT NP_BIND 117 120 GTP (BY SIMILARITY).
 FT DOMAIN 34 42 GTP (BY SIMILARITY).
 FT LIPID 189 189 EFFECTOR REGION (POTENTIAL).

FT LIPID 189 189 GERANYL-GERANYL (BY SIMILARITY).
 SQ SEQUENCE 192 AA; 21661 MW; 669024366AA3AA21 CRC64;

Query Match 79.1%; Score 34; DB 1; Length 192;
 Best Local Similarity 100.0%; Pred. No. 61;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 CGKTC 6
 |||||
 DB 16 CGKTC 20

Search completed: May 6, 2003, 10:29:29
 Job time : 13 secs

AC 08T0H3;
 DT 01-JUN-2002 (TREMBlrel. 21, Created)
 DT 01-JUN-2002 (TREMBlrel. 21, Last sequence update)
 DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
 DE L003740P.
 GN P120CTN.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 RX NCBI_TaxID=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-BERKELEY;
 RA Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
 RA Champe M., Chavez C., Dorsett V., Farfan D., Frise E., George R.,
 RA Gonzalez M., Guartin H., Li P., Liao G., Miranda A., Mungall C.J.,
 RA Nunoo J., Paclebo J., Paragas V., Park S., Phouanavong S., Wan K.,
 RA Yu C., Lewis S.E., Rubin G.M., Celisner S.,
 RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY0659321; AAL39466.1;
 SQ SEQUENCE 562 AA; 62937 MW; 4FBC2C38370923C CRC64;

Query Match 90.7%; Score 39; DB 5; Length 562;
 Best Local Similarity 83.3%; Pred. No. 16;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 CCGKTC 6
 DB 153 CCGETC 158

RESULT 3

O9W5T9 PRELIMINARY; PRT; 779 AA.

DT 01-MAY-2000 (TREMBlrel. 13, Created)
 DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
 DE Putative P120CTN protein (CG17484 protein).
 GN P120CTN OR CG17484.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 RX NCBI_TaxID=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-BERKELEY;
 RA MEDLINE=20196006; PubMed=10731132;
 RA Adams M.D., Celisner S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
 RA Abail J.F., Agbayani A., An H.-J., Andrews-Pfannkuch C., Baldwin D.,
 RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.V., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
 RA Borokova D., Botchan M.R., Bouck J., Brokstein P., Brotlier P.,
 RA Butlis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Dudin K.J., Evangelista C.C., Ferraz C., Fertiera S., Fleischmann W.,
 RA Foster C., Gabrielian A.E., Gang N.S., Gelbart W.M., Glasser K.,
 RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.H., Ibegwan C.,
 RA Jajali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp J., Lai Z.,
 RA Laasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,

RA Merkulov G., Mishina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon R., Nussken D.R., Paclebo J.M.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Klimos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.,
 RL The genome sequence of Drosophila melanogaster.
 DR EMBL; AE002751; AAF45461.1;
 DR HSSP; P35222; 1631.
 DR P120CTN OR CG17484.
 DR FlyBase; FBgn0015587; p120ctn.
 DR InterPro; IPR000225; Armadillo.
 DR Pfam; PF00514; Armadillo_seg; 4.
 DR SMART; SM00185; ARM; 3.
 DR PROSITE; PSS0176; ARM_REPEAT; 3.
 KW Hypothetical protein.

Query Match 90.7%; Score 39; DB 5; Length 779;
 Best Local Similarity 83.3%; Pred. No. 21;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 CCGKTC 6
 DB 340 CCGETC 345

RESULT 4

O9NHPI PRELIMINARY; PRT; 781 AA.

DT 01-OCT-2000 (TREMBlrel. 15, Created)
 DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
 DE Putative P120CTN protein (CG17484 protein).
 GN P120CTN OR CG17484.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 RX NCBI_TaxID=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC Cavallo R., Myster S., Pelfer M.,
 RA "A Drosophila melanogaster homolog of the adherens junction protein
 RT p120ctn."
 RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF220496; AAF33245.1;
 DR HSSP; P35222; 1631.
 DR FlyBase; FBgn0015587; p120ctn.
 DR InterPro; IPR000225; Armadillo.
 DR Pfam; PF00514; Armadillo_seg; 5.
 DR SMART; SM00185; ARM; 3.
 DR PROSITE; PSS0176; ARM_REPEAT; 3.
 SQ SEQUENCE 781 AA; 86836 MW; 5A1F546AE055CC2B CRC64;

Query Match 90.7%; Score 39; DB 5; Length 781;
 Best Local Similarity 83.3%; Pred. No. 21;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 CCGKTC 6
 DB 372 CCGETC 377

RESULT 5

09GNM6
ID 09GNM6 PRELIMINARY; PRT: 196 AA.
AC 09GNM6;
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Putative cathepsin B.5 (Fragment).
GN CATB.5.
OS Osterlagia osterlagi.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Strongylida;
OC Trichostrongyloidea; Haemonchidae; Osterlagiinae; Osterlagia.
OX NCBI_TaxID=6317;
RN [1]
RP SEQUENCE FROM N.A.
RA Geldhof P.B., Vercouteren I.J.R., Peelers I., Agnassens J.,
RA Claerebout E., Vercruysse J.;
RT *Molecular and biochemical characterization of cathepsin B enzymes in
RT Osterlagia osterlagi.*;
RL Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AJ296148; CAC13131.1; -
DR HSP68; IQDQ.
DR InterPro: IPR000668; Peptidase_C1.
DR InterPro: IPR001230; Prenyl.site.
DR InterPro: IPR000169; SHprot.acsite.
DR Pfam: PF00112; Peptidase_C1; 1.
DR ProDom: PD000158; Peptidase_C1; 1.
DR PROSITE: PS00294; PRENYLATION; UNKNOWN_1.
DR PROSITE: PS00639; THIOL_PROTEASE_HIS; 1.
FT NON_TER 1
FT 196
SQ SEQUENCE 196 AA; 21114 MW; F2B57E2885EB2DF2 CRC64;
Query Match
Best Local Similarity 86.0%; Score 37; DB 5; Length 196;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OY 1 CCGKTC 6
DB 35 CCGKRC 40
RESULT 6
O96LP4 PRELIMINARY; PRT: 205 AA.
ID 096LP4;
AC 096LP4;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE CDNA FLJ25328 f1s, clone TST00484.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=TESTIS;
RA Ishihashi T., Kanehori K., Yosida M., Watanabe S., Ishida S., Ono Y.,
RA Hota T., Hiraoka S., Murakawa K., Takiguchi S., Kusano J.,
RA Watanabe M., Fujimori K., Tanai H., Ishida M., Yamashita H., Chiba Y.,
RA Suzuki Y., Hata H., Nakagawa K., Mizuno S., Morinaga M., Kawamura M.,
RA Sugiyama T., Irie R., Otsuki T., Sato H., Nishikawa T., Sugiyama A.,
RA Kawakami B., Nagai K., Isogai T., Suga S.;
RT *NEO human cDNA sequencing project.*;
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AK058057; BAB71644.1; -
SQ SEQUENCE 205 AA; 21968 MW; 91543A18215F94F CRC64;
Query Match
Best Local Similarity 86.0%; Score 37; DB 4; Length 205;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OY 1 CCGKTC 6
DB 11111

DB 50 CCGKOC 55
RESULT 7
O29897 PRELIMINARY; PRT: 211 AA.
ID 029897;
AC 029897;
DT 01-JAN-1998 (TREMBLrel. 05, Created)
DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE Conserved hypothetical transmembrane protein.
GN AF0350.
OS Archaeoglobus fulgidus.
OC Archaea; Euryarchaeota; Archaeoglobi; Archaeoglobales;
OC Archaeoglobaceae; Archaeoglobus.
OX NCBI_TaxID=2234;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=VC-16 / DSM 4304 / ATCC 49558;
RX MEDLINE=98049343; PubMed=9389475;
RA Klein H.-P., Clayton R.A., Tomb J.-F., White O., Nelson K.E.,
RA Kelchum K.A., Dodson R.A., Gwin M., Hickey E.K., Peterson J.D.,
RA Richardson D.L., Kervatage A.R., Graham D.E., Kyriades N.C.,
RA Fleischmann R.D., Quackenbush J., Lee N.H., Sutton G.G., Gill S.,
RA Kirschner E.F., Dougherty B.A., McKenney K., Adams M.D., Loftus B.,
RA Peterson S., Reich C.I., McNeil L.K., Badger J.H., Glodok A., Zhou L.,
RA Overbeek R., Gocayne J.D., Weidman J.F., McDonald L., Utterback T.,
RA Cotton M.D., Sprites T., Artlich P., Kaine B.P., Sykes S.M.,
RA Sadow P.W., D'Andrea K.P., Bowman C., Fujii C., Garland S.A.,
RA Mason T.M., Olsen G.J., Fraser C.M., Smith H.O., Woese C.R.,
RA Venter J.C.;
RT *The complete genome sequence of the hyperthermophilic, sulphate-
RT reducing archaeon Archaeoglobus fulgidus.*;
RL Nature 390:364-370(1997).
DR EMBL: AE001080; AAB90884.1; -
DR TIGR: AF0350;
DR InterPro: IPR002781; DUF81.
DR Pfam: PF01925; DUF81; 1.
KW Hypothetical protein; Transmembrane; Complete proteome.
SQ SEQUENCE 211 AA; 23303 MW; 927825BC1EFC1B46 CRC64;
Query Match
Best Local Similarity 86.0%; Score 37; DB 17; Length 211;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OY 1 CCGKTC 6
DB 80 CCGKRC 85
RESULT 8
O9TXT4 PRELIMINARY; PRT: 217 AA.
ID 09TXT4;
AC 09TXT4;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE Hypothetical 24.4 kDa protein.
GN F53C3.5.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditioidea;
OC Rhabditidae; Pelodierinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BRISTOL N2;
RX MEDLINE=99069613; PubMed=9851916;
RA None;
RT *Genome sequence of the nematode C. elegans: a platform for
RT investigating biology. The C. elegans Sequencing Consortium.*;
RL Science 282:2012-2018(1998).
RN [2]
RP SEQUENCE FROM N.A.

RC STRAIN-BRISTOL NZ;
 RA Murray J., Wohlmann P., Bauer C., Antoniou B.;
 RT "The sequence of C. elegans cosmid F53C3.";
 RL Submitted (OCT-1998) to the EMBL/Genbank/DBJ databases.
 RN [13]
 RP SEQUENCE FROM N.A.
 RC STRAIN-BRISTOL NZ;
 RA Waterston R.;
 RT "Direct Submission.";
 RL Submitted (SEP-2001) to the EMBL/Genbank/DBJ databases.
 DR EMBL: AF098992; AAC67456.1; -
 DR InterPro: IPR002619; CX.
 DR Pfam: PF01705; CX; 1.
 DR ProDom: PD006744; CX; 1.
 KW Hypothetical protein.
 SQ SEQUENCE 217 AA; 24433 MW; 03BF85067036933C CRC64;
 SO
 Query Match 86.0%; Score 37; DB 5; Length 217;
 Best Local Similarity 83.3%; Pred. NO. 17;
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 CCGKTC 6
 DB 132 CCGMTC 137
 RESULT 9
 Q69285 PRELIMINARY; PRT; 270 AA.
 AC Q69285;
 DT 01-NOV-1996 (TREMBLrel. 01, Created)
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
 DE US2 protein.
 GN US2.
 OS Turkey herpesvirus.
 CC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
 CC Alphaherpesvirinae; Marek's disease-like viruses.
 OK NCBI_TaxID=10390;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=9513166; PubMed=7831788;
 RA Brunovskis P., Velicer L.F.;
 RT "The Marek's disease virus (MDV) unique short region: alpha herpesvirus-homologous, fowlpox virus-homologous, and MDV-specific genes.";
 RL Virology 206:324-338(1995).
 DR EMBL: L22174; AAA64964.1; -
 DR InterPro: IPR000169; SHprot_acsite.
 DR InterPro: IPR003485; US2_Unk.
 DR Pfam: PF02476; US2; 1.
 DR PROSITE: PS00639; THIOI_PROTEASE_HIS; UNKNOWN.1.
 SQ SEQUENCE 270 AA; 29735 MW; 47F36676BED75B74 CRC64;
 SO
 Query Match 86.0%; Score 37; DB 12; Length 270;
 Best Local Similarity 83.3%; Pred. NO. 20;
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 CCGKTC 6
 DB 234 CCGKCC 239
 RESULT 10
 Q9E6L9 PRELIMINARY; PRT; 270 AA.
 AC Q9E6L9;
 DT 01-MAR-2001 (TREMBLrel. 16, Created)
 DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
 DE HSV1 US2.
 GN MDV091.
 OS Turkey herpesvirus.

OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
 OC Alphaherpesvirinae; Marek's disease-like viruses.
 OK NCBI_TaxID=10390;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-MDS;
 RX MEDLINE=20392152; PubMed=10933706;
 RA Tulman E.R., Afonso C.L., Lu Z., Zsak L., Rock D.L., Kutish G.F.;
 RT "The genome of a very virulent Marek's disease virus.";
 RL J. Virol. 74:7980-7988(2000).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-MDS;
 RA Tulman E.R., Afonso C.L., Lu Z., Zsak L., Rock D.L., Kutish G.F.;
 RL Submitted (MAR-2000) to the EMBL/Genbank/DBJ databases.
 DR EMBL: AF243438; AAG14265.1; -
 DR InterPro: IPR000169; SHprot_acsite.
 DR InterPro: IPR003485; US2_Unk.
 DR Pfam: PF02476; US2; 1.
 DR PROSITE: PS00639; THIOI_PROTEASE_HIS; UNKNOWN.1.
 SQ SEQUENCE 270 AA; 29848 MW; A5556D8E872E731F CRC64;
 SO
 Query Match 86.0%; Score 37; DB 12; Length 270;
 Best Local Similarity 83.3%; Pred. NO. 20;
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 CCGKTC 6
 DB 234 CCGKCC 239
 RESULT 11
 Q8SZU1 PRELIMINARY; PRT; 407 AA.
 AC Q8SZU1;
 DT 01-JUN-2002 (TREMBLrel. 21, Created)
 DT 01-JUN-2002 (TREMBLrel. 21, Last sequence update)
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
 DE GH10778P.
 OS Drosophila melanogaster (Fruit fly).
 CC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 CC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 CC Ephydriodea; Drosophilidae; Drosophila.
 OK NCBI_TaxID=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-BERKELEY;
 RA Stapleton M., Brokstein P., Hong L., Aghayani A., Carlson J.,
 RA Champagne M., Chavez C., Dorsett V., Dresner D., Farfan D., Frise E.,
 RA George R., Gonzalez M., Guarin H., Krommiller B., Li P., Liao G.,
 RA Miranda A., Mungall C.J., Nunoo J., Pacle J., Paragas V., Park S.,
 RA Patel S., Phoumanavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,
 RA Ceiliker S.;
 RL Submitted (DEC-2001) to the EMBL/Genbank/DBJ databases.
 DR EMBL: AY070508; AAL47979.1; -
 SQ SEQUENCE 407 AA; 46046 MW; 4CF766081CEDC60F CRC64;
 SO
 Query Match 86.0%; Score 37; DB 5; Length 407;
 Best Local Similarity 83.3%; Pred. NO. 28;
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 CCGKTC 6
 DB 349 CCGKCC 354
 RESULT 12
 Q9J3E9 PRELIMINARY; PRT; 4467 AA.
 AC Q9J3E9;
 DT 01-OCT-2000 (TREMBLrel. 15, Created)
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)

DE RNA-directed RNA polymerase.
 OS murine hepatitis virus.
 OC Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;
 OC Coronaviridae; Coronavirus.
 OX NCBI_TaxID-11138;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-MV-10;
 RA Das Sarma J., Hingley S.T., Lai M.M.C., Weiss S.R., Lavi E.;
 RT "Pathogenesis and sequence analysis of mouse hepatitis virus type 2;
 RT an experimental model system of acute meningitis and hepatitis in
 RT mice."
 RT Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
 RL EMBL: AF208067; AAF69341.1; -
 DR MEROPS: C30.001; -
 DR MEROPS: C30.001; -
 DR InterPro: IPR002589; Peptidase_C16.
 DR InterPro: IPR002705; Peptidase_C16.
 DR InterPro: IPR000504; RNA_rec_mot.
 DR Pfam: PF0161; Alpp; 1.
 DR Pfam: PF01831; Peptidase_C16; 1.
 DR SMART: SM00506; Alpp; 1.
 DR PROSITE: PS00030; RRM_RNP_1; UNKNOWN_1.
 DR RNA-directed RNA polymerase.
 KM SEQUENCE 4467 AA; 496337 MW; 0F4CD64E7E2D7146 CRC64;
 SQ

Query Match 86.0%; Score 37; DB 12; Length 4467;
 Best Local Similarity 83.3%; Pred. No. 2.1e+02;
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 CCGKTC 6
 DB 387 CCGDTC 392

RESULT 13
 ID 039225 PRELIMINARY; PRT; 4470 AA.
 AC 039225;
 DT 01-JAN-1998 (TREMBLrel. 05, Created)
 DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE RNA-directed RNA polymerase.
 OS murine hepatitis virus.
 OC Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;
 OC Coronaviridae; Coronavirus.
 OX NCBI_TaxID-11138;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-MHV-A59;
 RC MEDLINE-98087821; PubMed-9426441;
 RA Leparc-Goffart I., Hingley S.T., Chua M.M., Jiang X., Lavi E.,
 RA Weiss S.R.;
 RT "Altered pathogenesis of a mutant of the murine coronavirus MHV-A59 is
 RT associated with a Q159L amino acid substitution in the spike
 RT protein."
 RT Virology 239:1-10(1997).
 RL [2]
 RN SEQUENCE FROM N.A.
 RC STRAIN-MHV-A59;
 RA Weiss S.R., Leparc-Goffart I., Hingley S.T.;
 RL Submitted (OCT-1997) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF029248; AAB86820.1; -
 DR InterPro: IPR002589; Alpp.
 DR InterPro: IPR002705; Peptidase_C16.
 DR Pfam: PF0161; Alpp; 1.
 DR Pfam: PF01831; Peptidase_C16; 1.
 DR SMART: SM00506; Alpp; 1.
 DR RNA-directed RNA polymerase.
 KM SEQUENCE 4470 AA; 496513 MW; 8DEE7E9BDF663FAF CRC64;
 SQ

Query Match 86.0%; Score 37; DB 12; Length 4470;
 Best Local Similarity 83.3%; Pred. No. 2.1e+02;

Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 OY 1 CCGKTC 6
 DB 390 CCGDTC 395

RESULT 14
 ID 09BPA0 PRELIMINARY; PRT; 83 AA.
 AC 09BPA0;
 DT 01-JUN-2001 (TREMBLrel. 17, Created)
 DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE Conotoxin scaffold VI/VII.
 OS Conus ventricosus (Mediterranean cone).
 OC Eukaryota; Metazoa; Mollusca; Gastropoda; Caenogastropoda;
 OC Neogastropoda; Conoidea; Conidae; Conus.
 OX NCBI_TaxID-117992;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-21105969; PubMed-1158371;
 RA Conticello S.G., Gilad Y., Avidan N., Ben-Asher E., Levy Z.,
 RA Fainzilber M.;
 RT "Mechanisms for Evolving Hypervariability: The Case of Conopeptides."
 RT Mol. Biol. Evol. 18:120-131(2001).
 RL EMBL: AF215037; AAG60465.1; -
 DR EMBL: AF215037; AAG60465.1; -
 DR InterPro: IPR004214; Conotoxin.
 DR Pfam: PF02950; Conotoxin; 1.
 DR SEQUENCE 83 AA; 9403 MW; D53923EACAE1974 CRC64;
 SQ

Query Match 83.7%; Score 36; DB 5; Length 83;
 Best Local Similarity 83.3%; Pred. No. 11;
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 CCGKTC 6
 DB 73 CCGGTC 78

RESULT 15
 ID 061515 PRELIMINARY; PRT; 348 AA.
 AC 061515;
 DT 01-AUG-1998 (TREMBLrel. 07, Created)
 DT 01-AUG-1998 (TREMBLrel. 07, Last sequence update)
 DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
 DE Cathepsin B-like cysteine protease GCP7.
 GN GCP7.
 OS Haemonchus contortus (Barber pole worm).
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Strongylida;
 OC Trichostrongyloidea; Haemonchidae; Haemonchinae; Haemonchus.
 OX NCBI_TaxID-6289;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-OSDA BELTSVILLE; TISSUE-INTESTINE;
 RA Rehman A., Jasmer D.P.;
 RL Submitted (FEB-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF046229; AAC05262.1; -
 DR HSP: P07688; IODQ.
 DR MEROPS: C01.101; -
 DR InterPro: IPR000668; Peptidase_C1.
 DR InterPro: IPR000169; SHprot_acsite.
 DR Pfam: PF00112; Peptidase_C1; 1.
 DR PRINTS: PR00705; PAPAIN.
 DR PRODOM: PD000158; Peptidase_C1; 1.
 DR PROSITE: PS00139; THIOL_PROTEASE_CYS; UNKNOWN_1.
 DR PROSITE: PS00639; THIOL_PROTEASE_HIS; UNKNOWN_1.
 DR PROTEASE.
 KM SEQUENCE 348 AA; 39176 MW; 6AFD85F084B5DF5 CRC64;
 SQ

Query Match 83.7%; Score 36; DB 5; Length 348;
 Best Local Similarity 83.3%; Pred. No. 38;

Matches	5;	Conservative	0;	Mismatches	1;	Indels	0;	Gaps	0;
QY	1	CCGKTC	6						
Db	157	CCGKFC	162						

Search completed: May 6, 2003, 10:31:02
Job time : 88 secs

1	43	100.0	6	19	US-09-555-115A-66	Sequence 66, April
2	43	100.0	103	16	US-09-370-767-34140	Sequence 34140, A
3	43	100.0	103	16	US-09-270-767-49357	Sequence 49357, A
4	43	100.0	103	16	US-09-370-8499-180217	Sequence 180217, A
5	39	90.7	121	20	US-09-688-052-3216	Sequence 3216, April
6	39	90.7	475	16	US-09-270-767-46709	Sequence 46709, A

7	39	90.7	561	16	US-09-370-767-42679	Sequence 42679, App1
8	39	90.7	672	16	US-09-370-767-46165	Sequence 46165, App1
9	39	90.7	779	20	US-09-614-150-25746	Sequence 25746, App1
10	39	90.7	779	21	US-09-791-537-81601	Sequence 81601, App1
11	39	90.7	779	27	US-60-191-637-25876	Sequence 25876, App1
12	39	90.7	779	27	US-60-191-681-20485	Sequence 20485, App1
13	39	90.7	781	21	US-09-791-537-104827	Sequence 104827, App1
14	38	88.4	232	1	PCT-US99-08604-28	Sequence 28, App1
15	38	88.4	232	16	US-09-298-102-28	Sequence 28, App1
16	37	86.0	27	1	PCT-US01-223041A-131	Sequence 131, App1
17	37	86.0	27	1	PCT-US01-223041A-354	Sequence 354, App1
18	37	86.0	27	23	US-09-910-082A-131	Sequence 131, App1
19	37	86.0	31	23	US-09-910-082A-354	Sequence 354, App1
20	37	86.0	31	24	US-10-072-602B-154	Sequence 154, App1
21	37	86.0	31	24	US-10-072-602B-572	Sequence 572, App1
22	37	86.0	39	20	US-09-611-197-139	Sequence 139, App1
23	37	86.0	72	1	PCT-US01-223041A-130	Sequence 130, App1
24	37	86.0	72	23	US-09-910-082A-130	Sequence 130, App1
25	37	86.0	76	24	US-10-072-602B-153	Sequence 153, App1
26	37	86.0	102	1	PCT-US01-22971-159	Sequence 159, App1
27	37	86.0	102	1	PCT-US02-08123-1416	Sequence 1416, App1
28	37	86.0	102	1	PCT-US02-08123-1792	Sequence 1792, App1
29	37	86.0	102	1	PCT-US02-08124-585	Sequence 585, App1
30	37	86.0	102	1	PCT-US02-08124-740	Sequence 740, App1
31	37	86.0	102	1	PCT-US02-08276-439	Sequence 439, App1
32	37	86.0	102	1	PCT-US02-08276-561	Sequence 561, App1
33	37	86.0	102	1	PCT-US02-08277-920	Sequence 920, App1
34	37	86.0	102	1	PCT-US02-08277-1170	Sequence 1170, App1
35	37	86.0	102	1	PCT-US02-08278-1357	Sequence 1357, App1
36	37	86.0	102	1	PCT-US02-08278-1719	Sequence 1719, App1
37	37	86.0	102	1	PCT-US02-09875-781	Sequence 781, App1
38	37	86.0	102	1	PCT-US02-09875-995	Sequence 995, App1
39	37	86.0	102	25	US-10-103-995-159	Sequence 159, App1
40	37	86.0	103	1	PCT-US01-00911-158	Sequence 158, App1
41	37	86.0	103	1	PCT-US99-15849-158	Sequence 158, App1
42	37	86.0	103	18	US-09-482-273-158	Sequence 158, App1
43	37	86.0	103	23	US-09-484-271-158	Sequence 158, App1
44	37	86.0	103	23	US-09-484-276-158	Sequence 158, App1
45	37	86.0	151	21	US-09-791-537-80760	Sequence 80760, App1

RESULT 1
US-09-555-115A-66
Sequence 66, Application US/09555115A

```

1  APPLICANT: Bohach, Gregory I.
2  TITLE OF INVENTION: NON-TOXIC IMMUNE STIMULATING ENTEROTOXIN COMPOSITIONS
3  FILE REFERENCE: 12136, 1USMO
4  CURRENT APPLICATION NUMBER: US/09/555,115A
5  CURRENT FILING DATE: 2000-08-01
6  PRIOR APPLICATION NUMBER: PCT/US98/25107
7  PRIOR FILING DATE: 1998-12-01
8  PRIOR APPLICATION NUMBER: US 60/067,357
9  PRIOR FILING DATE: 1997-12-02
10 NUMBER OF SEQ ID NOS: 66
11 SOFTWARE: PatentIn version 3.1
12 SEQ ID NO 66
13 LENGTH: 6
14 TYPE: prt
15 ORGANISM: Artificial Sequence
16 FEATURE:
17 OTHER INFORMATION: Synthetic
18 US-09-555-115A-66

```

Query Match	100.0%	Score 43;	DB 19;	Length 6;
Best Local Similarity	100.0%	Pred. No. 4.2e+06;		
Matches	6;	Conservative	0;	Mismatches 0;
				Indels 0;
				Gaps 0;
OY	1	CCGKTC	6	

Db 1 CCGKTC 6

RESULT 2
US-09-270-767-34140

Sequence 34140, Application US/09270767

GENERAL INFORMATION:

APPLICANT: Homburger et al.

TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster

FILE REFERENCE: File Reference: 7326-094

CURRENT APPLICATION NUMBER: US/09/270,767

CURRENT FILING DATE: 1999-03-17

NUMBER OF SEQ ID NOS: 62517

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 34140

LENGTH: 103

TYPE: PRT

ORGANISM: Drosophila melanogaster

US-09-270-767-34140

Query Match

Best Local Similarity 100.0%; Score 43; DB 16; Length 103;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 CCGKTC 6

Db 87 CCGKTC 92

RESULT 3
US-09-270-767-49357

Sequence 49357, Application US/09270767

GENERAL INFORMATION:

APPLICANT: Homburger et al.

TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster

FILE REFERENCE: File Reference: 7326-094

CURRENT APPLICATION NUMBER: US/09/270,767

CURRENT FILING DATE: 1999-03-17

NUMBER OF SEQ ID NOS: 62517

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 49357

LENGTH: 103

TYPE: PRT

ORGANISM: Drosophila melanogaster

US-09-270-767-49357

Query Match

Best Local Similarity 100.0%; Score 43; DB 16; Length 103;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 CCGKTC 6

Db 87 CCGKTC 92

RESULT 4
US-09-270-849B-180217

Sequence 180217, Application US/09270849B

GENERAL INFORMATION:

APPLICANT: Swimmer et al.

TITLE OF INVENTION: Insect genome survey devices

FILE REFERENCE:

CURRENT APPLICATION NUMBER: US/09/270,849B

CURRENT FILING DATE: 1999-03-17

NUMBER OF SEQ ID NOS: 195450

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 180217

LENGTH: 103

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Description of Artificial Sequence: Synthetic

Query Match
Best Local Similarity 100.0%; Score 43; DB 16; Length 103;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 CCGKTC 6

Db 87 CCGKTC 92

RESULT 5
US-09-688-052-3216

Sequence 3216, Application US/09688052

GENERAL INFORMATION:

APPLICANT: ALEXANDROV, Nikolai

TITLE OF INVENTION: Sequence-determined DNA Fragments and Corresponding Polypeptide

FILE REFERENCE: 2750-1238P

CURRENT APPLICATION NUMBER: US/09/688,052

CURRENT FILING DATE: 2000-10-13

NUMBER OF SEQ ID NOS: 4086

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 3216

LENGTH: 121

TYPE: PRT

ORGANISM: Arabidopsis thaliana

FEATURE:

NAME/KEY: misc.feature

LOCATION: 1..121

OTHER INFORMATION: Xaa is any amino acid

NAME/KEY: misc.feature

LOCATION: 1..121

OTHER INFORMATION: Ceres Seq. ID 1600282

US-09-688-052-3216

Query Match

Best Local Similarity 90.7%; Score 39; DB 20; Length 121;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Oy 1 CCGKTC 6

Db 94 CCGKTC 99

RESULT 6
US-09-270-767-46709

Sequence 46709, Application US/09270767

GENERAL INFORMATION:

APPLICANT: Homburger et al.

TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster

FILE REFERENCE: File Reference: 7326-094

CURRENT APPLICATION NUMBER: US/09/270,767

CURRENT FILING DATE: 1999-03-17

NUMBER OF SEQ ID NOS: 62517

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 46709

LENGTH: 475

TYPE: PRT

ORGANISM: Drosophila melanogaster

US-09-270-767-46709

Query Match

Best Local Similarity 90.7%; Score 39; DB 16; Length 475;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Oy 1 CCGKTC 6

Db 330 CCGKTC 335

RESULT 7
US-09-270-767-42679

Sequence 42679, Application US/09270767

DB 82 CCGTTC 87

RESULT 5

US-10-174-575-269
Sequence 269, Application US/10174575

GENERAL INFORMATION:

APPLICANT: Baker, Kevin P.
APPLICANT: Chen, Jian
APPLICANT: Desnoyers, Luc
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Pan, James
APPLICANT: Smith, Victoria
APPLICANT: Watanabe, Colin K.
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P3430R1C35
CURRENT FILING DATE: 2002-06-18
PRIOR APPLICATION NUMBER: 10/052586
PRIOR FILING DATE: 2002-01-15
PRIOR APPLICATION NUMBER: 60/059263
PRIOR FILING DATE: 1997-09-18
PRIOR APPLICATION NUMBER: 60/059266
PRIOR FILING DATE: 1997-09-18
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/063120
PRIOR FILING DATE: 1997-10-24
PRIOR APPLICATION NUMBER: 60/063121
PRIOR FILING DATE: 1997-10-24
PRIOR APPLICATION NUMBER: 60/063486
PRIOR FILING DATE: 1997-10-21
PRIOR APPLICATION NUMBER: 60/063540
PRIOR FILING DATE: 1997-10-28
PRIOR APPLICATION NUMBER: 60/063541
PRIOR FILING DATE: 1997-10-28
PRIOR APPLICATION NUMBER: 60/063544
PRIOR FILING DATE: 1997-10-28
Remaining Prior Application data removed - See file wrapper or PALM.
NUMBER OF SEQ ID NOS: 612
SEQ ID NO 269
LENGTH: 1300
TYPE: PRT
ORGANISM: Homo Sapien
US-10-174-575-269

Query Match

Best Local Similarity 86.0%; Score 37; DB 6; Length 1300;
Pred. No. 4.6e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 CCGKTC 6
DB 82 CCGTTC 87

RESULT 6

US-10-174-575A-269
Sequence 269, Application US/10174575A

GENERAL INFORMATION:

APPLICANT: Baker, Kevin P.
APPLICANT: Chen, Jian
APPLICANT: Desnoyers, Luc
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Pan, James
APPLICANT: Smith, Victoria

APPLICANT: Watanabe, Colin K.
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P3430R1C35
CURRENT FILING DATE: 2002-06-18
PRIOR APPLICATION NUMBER: 10/052586
PRIOR FILING DATE: 2002-01-15
PRIOR APPLICATION NUMBER: 60/059263
PRIOR FILING DATE: 1997-09-18
PRIOR APPLICATION NUMBER: 60/059266
PRIOR FILING DATE: 1997-09-18
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/063120
PRIOR FILING DATE: 1997-10-24
PRIOR APPLICATION NUMBER: 60/063121
PRIOR FILING DATE: 1997-10-24
PRIOR APPLICATION NUMBER: 60/063486
PRIOR FILING DATE: 1997-10-21
PRIOR APPLICATION NUMBER: 60/063540
PRIOR FILING DATE: 1997-10-28
PRIOR APPLICATION NUMBER: 60/063541
PRIOR FILING DATE: 1997-10-28
PRIOR APPLICATION NUMBER: 60/063544
PRIOR FILING DATE: 1997-10-28
Remaining Prior Application data removed - See file wrapper or PALM.
NUMBER OF SEQ ID NOS: 612
SEQ ID NO 269
LENGTH: 1300
TYPE: PRT
ORGANISM: Homo Sapien
US-10-174-575A-269

Query Match

Best Local Similarity 86.0%; Score 37; DB 6; Length 1300;
Pred. No. 4.6e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 CCGKTC 6
DB 82 CCGTTC 87

RESULT 7

US-10-187-755-269
Sequence 269, Application US/10187755

GENERAL INFORMATION:

APPLICANT: Baker, Kevin P.
APPLICANT: Chen, Jian
APPLICANT: Desnoyers, Luc
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Pan, James
APPLICANT: Smith, Victoria
APPLICANT: Watanabe, Colin K.
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P3430R1C1
CURRENT FILING DATE: 2002-07-01
PRIOR APPLICATION NUMBER: US/10/052,586
PRIOR FILING DATE: 2002-01-15
PRIOR APPLICATION NUMBER: 60/059263
PRIOR FILING DATE: 1997-09-18
PRIOR APPLICATION NUMBER: 60/059266
PRIOR FILING DATE: 1997-09-18
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17

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;; PRIOR APPLICATION NUMBER: 60/063120
;; PRIOR FILING DATE: 1997-10-24
;; PRIOR APPLICATION NUMBER: 60/063121
;; PRIOR FILING DATE: 1997-10-24
;; PRIOR APPLICATION NUMBER: 60/063486
;; PRIOR FILING DATE: 1997-10-21
;; PRIOR APPLICATION NUMBER: 60/063540
;; PRIOR FILING DATE: 1997-10-28
;; PRIOR APPLICATION NUMBER: 60/063541
;; PRIOR FILING DATE: 1997-10-28
;; PRIOR APPLICATION NUMBER: 60/063544
;; PRIOR FILING DATE: 1997-10-28
;; Remaining Prior Application data removed - See File Wrapper or PALM.
;; NUMBER OF SEQ ID NOS: 612
;; SEQ ID NO 269
;; LENGTH: 1300
;; TYPE: PRT
;; ORGANISM: Homo Sapien
US-10-187-749-269

Query Match      86.0%; Score 37; DB 6; Length 1300;
Best Local Similarity 83.3%; Pred. No. 4.6e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCGKTC 6
Db 82 CCGTTC 87

RESULT 8
US-10-187-749-269
;; Sequence 269, Application US/10187749
;; GENERAL INFORMATION:
;; APPLICANT: Baker, Kevin P.
;; APPLICANT: Chen, Jian
;; APPLICANT: Desnoyers, Luc
;; APPLICANT: Goddard, Audrey
;; APPLICANT: Godowski, Paul J.
;; APPLICANT: Gunney, Austin L.
;; APPLICANT: Pan, James
;; APPLICANT: Smith, Victoria
;; APPLICANT: Watanabe, Colin K.
;; APPLICANT: Wood, William I.
;; APPLICANT: Zhang, Zemin
;; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
;; FILE REFERENCE: P3430R1C1
;; CURRENT APPLICATION NUMBER: US/10/187,749
;; CURRENT FILING DATE: 2002-07-01
;; PRIOR APPLICATION NUMBER: US/10/052,586
;; PRIOR FILING DATE: 2002-01-15
;; PRIOR APPLICATION NUMBER: 60/059263
;; PRIOR FILING DATE: 1997-09-18
;; PRIOR APPLICATION NUMBER: 60/059266
;; PRIOR FILING DATE: 1997-09-18
;; PRIOR APPLICATION NUMBER: 60/062250
;; PRIOR FILING DATE: 1997-10-17
;; PRIOR APPLICATION NUMBER: 60/063120
;; PRIOR FILING DATE: 1997-10-24
;; PRIOR APPLICATION NUMBER: 60/063121
;; PRIOR FILING DATE: 1997-10-24
;; PRIOR APPLICATION NUMBER: 60/063486
;; PRIOR FILING DATE: 1997-10-21
;; PRIOR APPLICATION NUMBER: 60/063540
;; PRIOR FILING DATE: 1997-10-28
;; PRIOR APPLICATION NUMBER: 60/063541
;; PRIOR FILING DATE: 1997-10-28
;; PRIOR APPLICATION NUMBER: 60/063544
;; PRIOR FILING DATE: 1997-10-28
;; Remaining Prior Application data removed - See File Wrapper or PALM.
;; NUMBER OF SEQ ID NOS: 612
;; SEQ ID NO 269
;; LENGTH: 1300
;; TYPE: PRT
;; ORGANISM: Homo Sapien
US-10-187-749-269
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;; TYPE: PRT
;; ORGANISM: Homo Sapien
US-10-187-749-269

Query Match      86.0%; Score 37; DB 6; Length 1300;
Best Local Similarity 83.3%; Pred. No. 4.6e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCGKTC 6
Db 82 CCGTTC 87

RESULT 9
US-10-199-672-269
;; Sequence 269, Application US/10199672
;; GENERAL INFORMATION:
;; APPLICANT: Baker, Kevin P.
;; APPLICANT: Chen, Jian
;; APPLICANT: Desnoyers, Luc
;; APPLICANT: Goddard, Audrey
;; APPLICANT: Godowski, Paul J.
;; APPLICANT: Gunney, Austin L.
;; APPLICANT: Pan, James
;; APPLICANT: Smith, Victoria
;; APPLICANT: Watanabe, Colin K.
;; APPLICANT: Wood, William I.
;; APPLICANT: Zhang, Zemin
;; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
;; FILE REFERENCE: P3430R1C1
;; CURRENT APPLICATION NUMBER: US/10/199,672
;; CURRENT FILING DATE: 2002-07-18
;; PRIOR APPLICATION NUMBER: US/10/052,586
;; PRIOR FILING DATE: 2002-01-15
;; PRIOR APPLICATION NUMBER: 60/059263
;; PRIOR FILING DATE: 1997-09-18
;; PRIOR APPLICATION NUMBER: 60/059266
;; PRIOR FILING DATE: 1997-09-18
;; PRIOR APPLICATION NUMBER: 60/062250
;; PRIOR FILING DATE: 1997-10-17
;; PRIOR APPLICATION NUMBER: 60/063120
;; PRIOR FILING DATE: 1997-10-24
;; PRIOR APPLICATION NUMBER: 60/063121
;; PRIOR FILING DATE: 1997-10-24
;; PRIOR APPLICATION NUMBER: 60/063486
;; PRIOR FILING DATE: 1997-10-21
;; PRIOR APPLICATION NUMBER: 60/063540
;; PRIOR FILING DATE: 1997-10-28
;; PRIOR APPLICATION NUMBER: 60/063541
;; PRIOR FILING DATE: 1997-10-28
;; PRIOR APPLICATION NUMBER: 60/063544
;; PRIOR FILING DATE: 1997-10-28
;; Remaining Prior Application data removed - See File Wrapper or PALM.
;; NUMBER OF SEQ ID NOS: 612
;; SEQ ID NO 269
;; LENGTH: 1300
;; TYPE: PRT
;; ORGANISM: Homo Sapien
US-10-199-672-269

Query Match      86.0%; Score 37; DB 6; Length 1300;
Best Local Similarity 83.3%; Pred. No. 4.6e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCGKTC 6
Db 82 CCGTTC 87

RESULT 10
US-10-194-486-269
;; Sequence 269, Application US/10194486
```

```

; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3430R1C1
; CURRENT FILING DATE: 2002-07-11
; PRIOR APPLICATION NUMBER: US/10/052,586
; PRIOR FILING DATE: 2002-01-15
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059266
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063120
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063121
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063486
; PRIOR FILING DATE: 1997-10-21
; PRIOR APPLICATION NUMBER: 60/063540
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063541
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063544
; PRIOR FILING DATE: 1997-10-28
; Remaining prior Application data removed - See file Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 269
; LENGTH: 1300
; TYPE: PRT
; ORGANISM: Homo Sapien
; US-10-194-486-269

Query Match      86.0%; Score 37; DB 6; Length 1300;
Best Local Similarity 83.3%; Pred. No. 4.6e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy      1 CCGKTC 6
      |||||
Db      82 CCGTTC 87

RESULT 11
US-10-125-923A-451
; Sequence 451, Application US/10125923A
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3430R1C79
; CURRENT APPLICATION NUMBER: US/10/125,923A
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; CURRENT FILING DATE: 2002-01-15
; PRIOR APPLICATION NUMBER: 10/052586
; PRIOR FILING DATE: 2002-01-15
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059266
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063120
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063121
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063540
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063541
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063544
; Remaining prior Application data removed - See file Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 451
; LENGTH: 1743
; TYPE: PRT
; ORGANISM: Homo Sapien
; US-10-125-923A-451

Query Match      86.0%; Score 37; DB 6; Length 1743;
Best Local Similarity 83.3%; Pred. No. 5.7e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy      1 CCGKTC 6
      |||||
Db      1187 CCGATC 1192

RESULT 12
US-10-205-892-451
; Sequence 451, Application US/10205892
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3430R1C517
; CURRENT APPLICATION NUMBER: US/10/205,892
; CURRENT FILING DATE: 2002-07-26
; PRIOR APPLICATION NUMBER: 10/052586
; PRIOR FILING DATE: 2002-01-15
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059266
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063120
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063121
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063486
; PRIOR FILING DATE: 1997-10-21
; PRIOR APPLICATION NUMBER: 60/063540
```

```

: PRIOR FILING DATE: 1997-10-28
: PRIOR APPLICATION NUMBER: 60/063541
: PRIOR FILING DATE: 1997-10-28
: PRIOR APPLICATION NUMBER: 60/063544
: PRIOR FILING DATE: 1997-10-28
: Remaining Prior Application data removed - See File Wrapper or PALM.
: NUMBER OF SEQ ID NOS: 612
: SEQ ID NO 451
: LENGTH: 1743
: TYPE: PRT
: ORGANISM: Homo Sapien
US-10-205-892-451

Query Match      86.0%; Score 37; DB 6; Length 1743;
Best Local Similarity 83.3%; Pred. No. 5.7e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy      1 CCGKTC 6
Db      1187 CCGATC 1192

RESULT 13
US-10-174-575-451
: Sequence 451, Application US/10174575
: GENERAL INFORMATION:
: APPLICANT: Baker, Kevin P.
: APPLICANT: Chen, Jian
: APPLICANT: Desnoyers, Luc
: APPLICANT: Goddard, Audrey
: APPLICANT: Godowski, Paul J.
: APPLICANT: Gurney, Austin L.
: APPLICANT: Pan, James
: APPLICANT: Smith, Victoria
: APPLICANT: Watanabe, Colin K.
: APPLICANT: Wood, William I.
: APPLICANT: Zhang, Zemin
: TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
: FILE REFERENCE: P3430R1C35
: CURRENT FILING DATE: 2002-06-18
: PRIOR FILING DATE: 1997-09-18
: PRIOR APPLICATION NUMBER: 60/052586
: PRIOR FILING DATE: 2002-01-15
: PRIOR APPLICATION NUMBER: 60/059263
: PRIOR FILING DATE: 1997-09-18
: PRIOR APPLICATION NUMBER: 60/059266
: PRIOR FILING DATE: 1997-09-18
: PRIOR APPLICATION NUMBER: 60/062250
: PRIOR FILING DATE: 1997-10-17
: PRIOR APPLICATION NUMBER: 60/063120
: PRIOR FILING DATE: 1997-10-24
: PRIOR APPLICATION NUMBER: 60/063121
: PRIOR FILING DATE: 1997-10-24
: PRIOR APPLICATION NUMBER: 60/063486
: PRIOR FILING DATE: 1997-10-21
: PRIOR APPLICATION NUMBER: 60/063540
: PRIOR FILING DATE: 1997-10-28
: PRIOR APPLICATION NUMBER: 60/063541
: PRIOR FILING DATE: 1997-10-28
: PRIOR APPLICATION NUMBER: 60/063544
: PRIOR FILING DATE: 1997-10-28
: Remaining Prior Application data removed - See File Wrapper or PALM.
: NUMBER OF SEQ ID NOS: 612
: SEQ ID NO 451
: LENGTH: 1743
: TYPE: PRT
: ORGANISM: Homo Sapien
US-10-174-575-451

Query Match      86.0%; Score 37; DB 6; Length 1743;
Best Local Similarity 83.3%; Pred. No. 5.7e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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```

Oy      1 CCGKTC 6
Db      1187 CCGATC 1192

RESULT 14
US-10-174-575A-451
: Sequence 451, Application US/10174575A
: GENERAL INFORMATION:
: APPLICANT: Baker, Kevin P.
: APPLICANT: Chen, Jian
: APPLICANT: Desnoyers, Luc
: APPLICANT: Goddard, Audrey
: APPLICANT: Godowski, Paul J.
: APPLICANT: Gurney, Austin L.
: APPLICANT: Pan, James
: APPLICANT: Smith, Victoria
: APPLICANT: Watanabe, Colin K.
: APPLICANT: Wood, William I.
: APPLICANT: Zhang, Zemin
: TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
: FILE REFERENCE: P3430R1C35
: CURRENT FILING DATE: 2002-06-18
: PRIOR FILING DATE: 2002-01-15
: PRIOR APPLICATION NUMBER: 60/052586
: PRIOR FILING DATE: 2002-01-15
: PRIOR APPLICATION NUMBER: 60/059263
: PRIOR FILING DATE: 1997-09-18
: PRIOR APPLICATION NUMBER: 60/059266
: PRIOR FILING DATE: 1997-09-18
: PRIOR APPLICATION NUMBER: 60/062250
: PRIOR FILING DATE: 1997-10-17
: PRIOR APPLICATION NUMBER: 60/063120
: PRIOR FILING DATE: 1997-10-24
: PRIOR APPLICATION NUMBER: 60/063121
: PRIOR FILING DATE: 1997-10-24
: PRIOR APPLICATION NUMBER: 60/063486
: PRIOR FILING DATE: 1997-10-21
: PRIOR APPLICATION NUMBER: 60/063540
: PRIOR FILING DATE: 1997-10-28
: PRIOR APPLICATION NUMBER: 60/063541
: PRIOR FILING DATE: 1997-10-28
: PRIOR APPLICATION NUMBER: 60/063544
: PRIOR FILING DATE: 1997-10-28
: Remaining Prior Application data removed - See File Wrapper or PALM.
: NUMBER OF SEQ ID NOS: 612
: SEQ ID NO 451
: LENGTH: 1743
: TYPE: PRT
: ORGANISM: Homo Sapien
US-10-174-575A-451

Query Match      86.0%; Score 37; DB 6; Length 1743;
Best Local Similarity 83.3%; Pred. No. 5.7e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy      1 CCGKTC 6
Db      1187 CCGATC 1192

RESULT 15
US-10-187-755-451
: Sequence 451, Application US/10187755
: GENERAL INFORMATION:
: APPLICANT: Baker, Kevin P.
: APPLICANT: Chen, Jian
: APPLICANT: Desnoyers, Luc
: APPLICANT: Goddard, Audrey
: APPLICANT: Godowski, Paul J.
: APPLICANT: Gurney, Austin L.
: APPLICANT: Pan, James
: APPLICANT: Smith, Victoria
: APPLICANT: Watanabe, Colin K.
: APPLICANT: Wood, William I.
: APPLICANT: Zhang, Zemin
: TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
: FILE REFERENCE: P3430R1C35
: CURRENT FILING DATE: 2002-06-18
: PRIOR FILING DATE: 2002-01-15
: PRIOR APPLICATION NUMBER: 60/052586
: PRIOR FILING DATE: 2002-01-15
: PRIOR APPLICATION NUMBER: 60/059263
: PRIOR FILING DATE: 1997-09-18
: PRIOR APPLICATION NUMBER: 60/059266
: PRIOR FILING DATE: 1997-09-18
: PRIOR APPLICATION NUMBER: 60/062250
: PRIOR FILING DATE: 1997-10-17
: PRIOR APPLICATION NUMBER: 60/063120
: PRIOR FILING DATE: 1997-10-24
: PRIOR APPLICATION NUMBER: 60/063121
: PRIOR FILING DATE: 1997-10-24
: PRIOR APPLICATION NUMBER: 60/063486
: PRIOR FILING DATE: 1997-10-21
: PRIOR APPLICATION NUMBER: 60/063540
: PRIOR FILING DATE: 1997-10-28
: PRIOR APPLICATION NUMBER: 60/063541
: PRIOR FILING DATE: 1997-10-28
: PRIOR APPLICATION NUMBER: 60/063544
: PRIOR FILING DATE: 1997-10-28
: Remaining Prior Application data removed - See File Wrapper or PALM.
: NUMBER OF SEQ ID NOS: 612
: SEQ ID NO 451
: LENGTH: 1743
: TYPE: PRT
: ORGANISM: Homo Sapien
US-10-187-755-451

Query Match      86.0%; Score 37; DB 6; Length 1743;
Best Local Similarity 83.3%; Pred. No. 5.7e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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APPLICANT: Pan,James
APPLICANT: Smith,Victoria
APPLICANT: Watanabe,Colin K.
APPLICANT: Wood,William I.
APPLICANT: Zhang,Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P3430R1C1
CURRENT APPLICATION NUMBER: US/10/187,755
CURRENT FILING DATE: 2002-07-01
PRIOR APPLICATION NUMBER: US/10/052,586
PRIOR FILING DATE: 2002-01-15
PRIOR APPLICATION NUMBER: 60/059263
PRIOR FILING DATE: 1997-09-18
PRIOR APPLICATION NUMBER: 60/059266
PRIOR FILING DATE: 1997-09-18
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/063120
PRIOR FILING DATE: 1997-10-24
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PRIOR FILING DATE: 1997-10-24
PRIOR APPLICATION NUMBER: 60/063486
PRIOR FILING DATE: 1997-10-21
PRIOR APPLICATION NUMBER: 60/063540
PRIOR FILING DATE: 1997-10-28
PRIOR APPLICATION NUMBER: 60/063541
PRIOR FILING DATE: 1997-10-28
PRIOR APPLICATION NUMBER: 60/063544
PRIOR FILING DATE: 1997-10-28
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 612
SEQ ID NO 451
LENGTH: 1743
TYPE: PRT
ORGANISM: Homo Saplen
US-10-187-755-451

Query Match 86.0%; Score 37; DB 6; Length 1743;
Best Local Similarity 83.3%; Pred. No. 5.7e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 CCGKTC 6
11111
Db 1187 CCGATC 1192

Search completed: May 6, 2003, 10:36:15
Job time : 87 secs

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Indexing Officer: RMEBRATE - REDA MEBRATE
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Dossier: 09555115

Legal Date: 10-16-2003

No.	Doccode	Number of pages
1	SRNT	536

Total number of pages: 536

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Order of re-scan issued on

